

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:01:07 ; Search time 2294.29 Seconds  
(without alignments)  
16536.624 Million cell

updates/sec

Title: US-09-902-759-38  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	1804.8	99.5	1816	6	AX191598	AX191598 Sequence
5	1760.4	97.1	1831	6	AX073678	AX073678 Sequence
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8	1171.4	64.6	1173	6	AX191588	AX191588 Sequence
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10	828.2	45.7	187960	9	AP000866	AP000866 Homo sapi
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36	54.2	3.0	153292	2	AP003635	AP003635 Oryza sat
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38	51	2.8	51	6	AX161199	AX161199 Sequence
39	51	2.8	51	6	AX161201	AX161201 Sequence
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Sauriscoscomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	TITLE	JOURNAL
1 (bases 1 to 1838) AUTHORS Hirata, K.-I., Ishida, T., Penta, K., Rezaee, M., Yang, E., Wohlgenuth, J. and Quatermous, T.	Cloning of an Immunoglobulin Family Adhesion Molecule Selectively Expressed by Endothelial Cells	J. Biol. Chem. 276 (19), 16223-16231 (2001)

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QY		

11279107  
2 (bases 1 to 1838)  
Quertermous, T., Ishida, T. and Hirata, K.-i.  
Direct Submission  
Submitted (15-MAR-2001) Cardiovascular Medicine, Stanford  
University, 300 Pasteur Drive, Falk CVRC, Stanford, CA  
94305-5406, USA

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Ddb	1321	AAGGATTGGGTCTC	TCTCCCTATAAGGTCACCTCTAGCACAGAGCGCTGAGTCATG	1380		
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	07-MAY-2001								
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ACCESSION		AF361746							
VERSION		AF361746.1	GI:13959017						
KEYWORDS									
SOURCE		human.							
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 REFERENCE 1 (bases 1 to 1816)  
 AUTHORS Kato, S. and Kimura, T.  
 TITLE Human proteins having hydrophobic domains and dnas encoding these proteins  
 JOURNAL Patent: WO 0149728-A 120 12-JUL-2001;  
 Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)  
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AX073678  
 LOCUS AX073678 1831 bp DNA linear PAT  
 06-FEB-2001  
 DEFINITION Sequence 12 from Patent WO0104264.  
 ACCESSION AX073678  
 VERSION AX073678.1 GI:12710099  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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TITLE Atherosclerosis-associated genes  
 JOURNAL Patent: WO 0104264-A 12 18-JAN-2001;  
 Incyte Genomics, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1. 1831  
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 ORIGIN  
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QY	179	ggggtgagtgccctcgccccctcgggggccagctgcaactgcaactgcccggccaa	238
Db	183	GGGGCTGAGTGCCCTCGCGCCCTCGGGCCAGCTGCAACTGCACTTGCCCGCCAA	242
QY	239	ccggttgaggcggtggaggaggagggagtggtgttcagcgtggttaacactgcacgg	298
Db	243	CCGTTGACGGCGTGGAGGGAGGGAGTGTGCTTCCAGCGTGTACACCTTGCACGG	302
QY	299	ggaggtgtcttcacccagccatggagggtgcccctttgtgatgtggttttcaaacagaa	358
Db	303	GGAGTGTCTTCATCCAGCCATGGGAGTGCCCTTTGTGATGTGGTCTTCAAAACAGAA	362
QY	359	agaaaaggagatcaggtgtgtcctacatcaatgggggtcacacaagaacacctggagt	418
Db	363	AGAAAAGGAGGATCAGGTGTGCTTCTACATCAATGGGGTTCACAAAGCAACCTGGAGT	422
QY	419	atccttggtactcattccatccctcccggaacctgtccctgcggtgaggggtctccagga	478
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QY	479	gaaagacttgccccctacagctgctccgtgaatgtgcaagacaacaaggcaaatctag	538
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BC016868	
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09-NOV-2001	
DEFINITION Homo sapiens, clone MGC:17599 IMAGE:3850665, mRNA, complete cds.	
ACCESSION BC016868	
VERSION BC016868.1 GI:16877212	
KEYWORDS MGC.	
SOURCE human.	
ORGANISM Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE 1 (bases 1 to 1734)	
AUTHORS Strausberg, R.	
TITLE Direct Submission	
JOURNAL Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT Contact: MGC help desk	
Email: cgapbs-re@mail.nih.gov	
Tissue Procurement: ATCC	
cDNA Library Preparation: Life Technologies, Inc.	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA	
94305	
Web site: http://www-shgc.stanford.edu	
Contact: (Dickson, Mark) mcd@paxil.stanford.edu	
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.	

Db	361	GAAGACTCTGGCCCTACAGCTGCTCCGGAATGTGCAAGACAACAAGGCAAAATCTAG	420	
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RESULT 7

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LOCUS					
13-JUN-2001					
DEFINITION	Macaca fascicularis brain cDNA clone:QtrA-11419, full insert sequence.				
ACCESSION	AB060855				
VERSION	AB060855.1	GI:13874503			
KEYWORDS	oligo capping; fis (full insert sequence).				
SOURCE	Macaca fascicularis adult male temporal lobe right cDNA to mRNA, clone lib:macaque brain cDNA library QtrA clone:QtrA-11419.				
ORGANISM	Macaca fascicularis				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae; Macaca.				
REFERENCE	1 (sites)				
AUTHORS	Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.				
TITLE	Isolation of full-length cDNA clones from macaque brain cDNA libraries				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1855)				
AUTHORS	Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.				

**† TITLE ,**  
**JOURNAL**  
**of**  
**Direct Submission**  
**Submitted (27-APR-2001) Katsuyuki Hashimoto, National Institute**  
**Infectious Diseases, Division of Genetic Resources; 23-1, Toyama**  
**1-chome, Shinjuku-ku, Tokyo 162-8640, Japan**  
**(E-mail: khashi@nih.go.jp,**  
**URL: <http://www.nih.go.jp/yoken/genebank/>,**  
**Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181)**

COMMENT	TOP10	Lab host:
	Vector: pMG18S-FL3 (Acc.No. AB009864)	
	R. Site1: DraIII (CACCCTGTG)	
	R. Site2: DraIII (CACCATGTG)	
	Description: 1st strand cDNA was primed with an oligo (dT) primer [AATGGCGCTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed	

to exclude fragments <1.5kb. The *Sfi*I-digested PCR product was cloned into distinct *Dra*III sites of pME18S-FL3. *Xho*I sites just outside the *Dra*III sites can be used to isolate the cDNA insert.

**Libraries** were constructed by oligo-capping method (Sugano et al., , Institute of Medical Science, University of Tokyo).

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Custom primer used for sequencing
( 5' end primer [CTTCTGCTCTAAAGCTGCG] ;
  3' end primer [CGACCTGCAGCTCGAGCACA] ) .
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ORIGIN

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12

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## RESULT 9

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08-MAY-2001  
DEFINITION Mus musculus endothelial cell-selective adhesion molecule (Esam)  
mRNA, complete cds.  
ACCESSION AF361882  
VERSION AF361882.1 GI:13991772  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Mus.  
REFERENCE 1 (bases 1 to 1840)  
AUTHORS Hirata,K.-I., Ishida,T., Penta,K., Rezaee,M., Yang,E.,  
Wohlgemuth,J. and Quertermous,T.  
TITLE Cloning of an immunoglobulin family adhesion molecule selectively  
expressed by endothelial cells  
JOURNAL J. Biol. Chem. 276 (19), 16223-16231 (2001)  
PUBMED 11279107  
REFERENCE 2 (bases 1 to 1840)  
AUTHORS Quertermous,T., Ishida,T. and Hirata,K.-I.  
TITLE Direct Submission  
JOURNAL Submitted (16-MAR-2001) Cardiovascular Medicine, Stanford  
University, 300 Pasteur Drive, Falk CVRC, Stanford, CA  
94305-5406, USA

## FEATURES

Location/Qualifiers

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 28-AUG-2001  
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 REFERENCE 1 (bases 1 to 187960)  
 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
 TITLE Homo sapiens genomic DNA  
 JOURNAL Published Only in Database (1999) In press  
 REFERENCE 2 (bases 1 to 187960)  
 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-DEC-1999) Masahira Hattori, The Institute of  
 Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045,  
 Japan  
 (E-mail:hattori@gscl.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,  
 Tel:81-45-503-9111, Fax:81-45-503-9170)  
 COMMENT On Aug 27, 2001 this sequence version replaced gi:9845041.  
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 ORIGIN

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 30-MAY-2000  
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VERSION AP000680.2 GI:8118868  
KEYWORDS HTG, HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE Homo sapiens DNA, clone: CMB9-25K9.  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 101458)  
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,  
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
Homo sapiens 101,458 genomic DNA of 11q24  
Published Only in DataBase (1999) In press  
2 (bases 1 to 101458)  
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,  
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (08-NOV-1999) Masahira Hattori, The Institute of  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
Kitasato Univ., 1-15-1 Kitasato, Sagami-hara, Kanagawa 228-8555,  
Japan (E-mail: hattori@gsc.riken.go.jp,  
URL: http://hgp.gsc.riken.go.jp/, Tel: 81-42-778-9923,  
Fax: 81-42-778-9924)  
On May 31, 2000 this sequence version replaced gi:6997554.

## COMMENT

----- Genome Center  
Center: RIKEN Genomic Sciences Center (GSC)  
Center code: RIKEN  
Web site: http://hgp.gsc.riken.go.jp/  
Contact: hattori@gsc.riken.go.jp  
----- Project Information  
Center project name: HumDraft11  
Center clone name: CMB9-25K9  
----- Summary Statistics  
Sequencing vector: PCR products; 100% of reads  
Chemistry: Dye-terminator ET-amersham; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 99733 bases at least Q40  
Consensus quality: 95050 bases at least Q30  
Consensus quality: 97741 bases at least Q20  
Insert size: 99058; sum-of-contigs  
Quality coverage: 4.65x in Q20 bases; sum-of-contigs  
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NOTE: This is a 'working draft' sequence. It currently consists  
of 25 contigs. The true order of the pieces is not known and their  
order in this sequence record is arbitrary. Gaps between the  
contigs are represented as runs N, but the exact sizes of the  
gaps are unknown. This record will be updated with the finished  
sequence as soon as it is available and the accession number will be  
preserved

1 9364 contig of 9364 bp in length  
9465 16830 contig of 7366 bp in length  
16931 23631 contig of 6701 bp in length  
23732 29864 contig of 6133 bp in length

49585 55550 contig of 5046 bp in length  
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55651 61139 contig of 5489 bp in length  
61240 65471 contig of 4232 bp in length  
65572 69042 contig of 3471 bp in length  
69143 73512 contig of 4370 bp in length  
73613 76146 contig of 2534 bp in length  
76247 79045 contig of 2799 bp in length  
79146 82078 contig of 2933 bp in length  
82179 83583 contig of 1405 bp in length  
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96052 97799 contig of 1748 bp in length  
97900 100121 contig of 2222 bp in length  
100222 101458 contig of 1237 bp in length  
Sequence updated (26-May-2000).

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 25 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 9364: contig of 9364 bp in length  
\* 9365 9464: gap of 100 bp  
\* 9465 16830: contig of 7366 bp in length  
\* 16831 16930: gap of 100 bp  
\* 16931 23631: contig of 6701 bp in length  
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\* 23732 29864: contig of 6133 bp in length  
\* 29865 29964: gap of 100 bp  
\* 29965 38284: contig of 8320 bp in length  
\* 38285 38384: gap of 100 bp  
\* 38385 44338: contig of 5954 bp in length  
\* 44339 44438: gap of 100 bp  
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\* 55651 61139: contig of 5489 bp in length  
\* 61140 61239: gap of 100 bp  
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\* 65472 65571: gap of 100 bp  
\* 65572 69042: contig of 3471 bp in length  
\* 69043 69142: gap of 100 bp  
\* 69143 73512: contig of 4370 bp in length  
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\* 79046 79145: gap of 100 bp

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QY 1760 gtgtgttttcatttgcataatttaataaagatacataatgtttgtatgaaaaa 1813  
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RESULT 12

AF277292 AF277292 736 bp mRNA linear PRI

LOCUS AF277292

03-AUG-2000

DEFINITION Homo sapiens C4orf1 mRNA.

ACCESSION AF277292

VERSION AF277292.1 GI:9664852

KEYWORDS human.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 736)

AUTHORS Sim,D.L.C., Yeo,W.M. and Chow,V.T.K.

TITLE The novel human HUEL gene (C4orf1) encodes a protein that shares homology with the DNA-binding domain of the XPA DNA repair protein and displays nuclear translocation in a cell cycle-dependent manner

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 736)

AUTHORS Chow,V.T.K., Sim,D.L.C. and Yeo,W.M.

TITLE Direct Submission

JOURNAL Submitted (13-JUN-2000) Microbiology, National University of Singapore, 5, Science Drive 2, Singapore 117597, Singapore

FEATURES Location/Qualifiers

source 1..736

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/tissue\_type="bone marrow"

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RESULT 13
AX136493
LOCUS AX136493 637 bp DNA linear PAT
30-MAY-2001
DEFINITION Sequence 415 from Patent EP1067182.
ACCESSION AX136493
VERSION AX136493.1 GI:14272897
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 637)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 415 10-JAN-2001;
Helix Research Institute (JP)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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BASE COUNT 116 a 202 c 185 g 129 t 5 others
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Query Match 29.3%; Score 531.2; DB 6; Length 637;
Best Local Similarity 95.8%; Pred. No. 8.9e-113;
Matches 576; Conservative 0; Mismatches 21; Indels 4; Gaps
3;
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Db 132 GGGCCATGATTTCCTCCCGGGGCCCTGGTGACCACTTGTGCGGTTTTGTCTCTGG 191
Qy 181 ggtgagtgccctgcgccccctcgcgggcccagctgcaactgcaactgcccgcgaacc 240
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BASE COUNT 118 a 118 c 96 g 109 t

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QY 1476 aaggagaagaggagtgatctggaattgggaggagcctccaccacccctgactctcc 1535

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Db 121 AAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCTCTCC 180

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QY 1776 caattttaataaagatacat 1796

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Search completed: August 19, 2002, 16:13:11

Job time: 4324 sec

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QY 1337 tccttcctataaagggtaccctctagcacagagccctgagtcattgggaaagagtcacactc 1396

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RESULT 15

LOCUS AX332845

441 bp DNA linear PAT

09-JAN-2002

DEFINITION Sequence 3354 from Patent WO0194629.

ACCESSION AX332845

VERSION AX332845.1 GI:18123479

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,

Horrigan,S., Soppet,D.R. and Weaver,Z.

TITLE Cancer gene determination and therapeutic screening using

signature

gene sets

JOURNAL Patent: WO 0194629-A 3354 13-DEC-2001;

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:04:12 ; Search time 220.41 Seconds  
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14122.616 Million cell updates/sec

Title: US-09-902-759-38

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1

AAx52221

ID AAX52221 standard; DNA; 1813 BP.

## ALIGNMENTS

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4	1813	100.0	1813	22	Human cDNA sequenc
5	1813	100.0	1813	22	PRO246 coding sequ
6	1813	100.0	1813	22	Nucleotide sequenc
7	1813	100.0	1813	22	Human PRO246 cDNA.
8	1813	100.0	1813	22	Human angiogenesis
9	1809	99.8	1821	22	Human cDNA encodin
10	1806.6	99.6	1827	22	Human shear stress
11	1804.8	99.5	1816	22	Human protein havi
12	1802	99.4	1954	21	cDNA encoding huma
13	1783.8	98.4	1932	21	Human secreted pro
14	1760.4	97.1	1831	22	Atherosclerosis-as
15	1757.6	96.9	1869	22	Human INTERCEPT 25
16	1756	96.9	1869	22	Human secreted pro
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21	1440.8	79.5	1748	22	Human polynucleoti
22	1376	75.9	1387	20	Human viral recept
23	1083.2	59.7	1290	20	Human secreted pro
24	1069.8	59.0	1110	22	Human INTERCEPT 25
25	1068.2	58.9	1110	22	Human secreted pro
26	1068.2	58.9	1110	22	Human secreted pro
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28	1068.2	58.9	1110	22	Human secreted pro
29	1010.4	55.7	1606	22	Human polynucleoti
30	863.2	47.6	1846	22	Murine secreted pr
31	861.6	47.5	1846	22	Murine INTERCEPT 2
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42	453	25.0	541	22	Primer specific fo
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45	208	11.5	533	22	Murine 7-transmemb

DT 25-JUN-1999 (first entry)  
 XX Protein PRO246 cDNA clone DNA35639-1172.  
 DE Secreted protein; transmembrane protein; human; enterocolitis;  
 XX Zollinger-Ellison syndrome; gastrointestinal ulceration;  
 KW congenital microvillus atrophy; skin disease; cell growth;  
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;  
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;  
 KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;  
 KW anti-thrombotic; wound healing; tissue repair; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09914328-A2.  
 XX  
 PD 25-MAR-1999.  
 XX  
 XX 16-SEP-1998; 98WO-US19330.  
 XX 25-NOV-1997; 97US-0066840.  
 PR 17-SEP-1997; 97US-0059113.  
 PR 17-SEP-1997; 97US-0059115.  
 PR 17-SEP-1997; 97US-0059117.  
 PR 17-SEP-1997; 97US-0059119.  
 PR 17-SEP-1997; 97US-0059121.  
 PR 17-SEP-1997; 97US-0059122.  
 PR 17-SEP-1997; 97US-0059184.  
 PR 18-SEP-1997; 97US-0059263.  
 PR 18-SEP-1997; 97US-0059266.  
 PR 15-OCT-1997; 97US-0062125.  
 PR 17-OCT-1997; 97US-0062285.  
 PR 17-OCT-1997; 97US-0062287.  
 PR 21-OCT-1997; 97US-0063486.  
 PR 24-OCT-1997; 97US-0062814.  
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 PR 24-OCT-1997; 97US-0063045.  
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 PR 24-OCT-1997; 97US-0063127.  
 PR 24-OCT-1997; 97US-0063128.  
 PR 27-OCT-1997; 97US-0063329.  
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 PR 28-OCT-1997; 97US-0063541.  
 PR 28-OCT-1997; 97US-0063542.  
 PR 28-OCT-1997; 97US-0063544.  
 PR 28-OCT-1997; 97US-0063549.  
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 PR 28-OCT-1997; 97US-0063564.  
 PR 29-OCT-1997; 97US-0063435.  
 PR 29-OCT-1997; 97US-0063704.  
 PR 29-OCT-1997; 97US-0063732.  
 PR 29-OCT-1997; 97US-0063738.  
 PR 29-OCT-1997; 97US-0063734.  
 PR 29-OCT-1997; 97US-0064215.

PR 03-NOV-1997; 97US-0064248.  
 PR 07-NOV-1997; 97US-0064809.  
 PR 12-NOV-1997; 97US-0065186.  
 PR 17-NOV-1997; 97US-0065846.  
 PR 18-NOV-1997; 97US-0065693.  
 PR 21-NOV-1997; 97US-0066120.  
 PR 21-NOV-1997; 97US-0066364.  
 PR 24-NOV-1997; 97US-0066772.  
 PR 24-NOV-1997; 97US-0066466.  
 PR 24-NOV-1997; 97US-0066770.  
 PR 24-NOV-1997; 97US-0066511.  
 PR 24-NOV-1997; 97US-0066453.

XX (GETH) GENENTECH INC.  
 PA  
 XX  
 PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;  
 XX  
 DR WPI; 1999-229533/19.  
 DR P-PSDB; AAY13351.  
 XX  
 PT New isolated human genes and polypeptides used in, e.g. treatment of  
 PT gastrointestinal ulceration  
 XX  
 PS Claim 2; Fig 16; 320pp; English.  
 XX  
 CC AAX52213-74 encode secreted and transmembrane human proteins, and are  
 CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,  
 CC fetal brain, fetal liver and fetal retina. The encoded polypeptides  
 CC have specific uses based on their homology to known polypeptides,  
 CC e.g. PRO211 and PRO217 can be used for disorders associated with the  
 CC preservation and maintenance of gastrointestinal mucosa and the repair  
 CC of acute and chronic mucosal lesions (e.g. enterocolitis,  
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital  
 CC microvillus atrophy), skin diseases associated with abnormal  
 CC keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as  
 CC lung squamous cell carcinoma of the vulva and gliomas), potent effects  
 on  
 CC cell growth and development, diseases related to growth or survival of  
 CC nerve cells including Parkinson's disease, Alzheimer's disease, ALS,  
 CC neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for  
 CC reducing dermal scarring. PRO264 can be used as a target for anti-tumor  
 CC drugs. PRO333 may be used in the treatment of Usher Syndrome or Atrophia  
 CC areata; PRO269 can be used as an anti-thrombotic agent; PRO287  
 CC polypeptides and portions may have therapeutic applications in wound  
 CC healing and tissue repair; PRO317 can be used for treating problems of  
 CC the kidney, uterus, endometrium, blood vessels, or related tissue, e.g.  
 CC in the heart of genital tract.  
 XX  
 SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 20; Length 1813;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 781 ctggagtcattgtctgcaaggcccaaatgaggtgggactgcccactgtaatgtgagcg 840  
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 Db 961 aggagccagccaatgatatacaaggaggatgcatgtctcccgagcctgcctggccca 1020  
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 Db 1021 agagctcagacacaaatctccaaagaatgggacccttctctgtcacctccgcacgagccc 1080  
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 Db 1141 gccaggccctgcctcaccaaagactgcccaagacagatggggcccaccctcaaccaatat 1200  
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Db	661	gtaagcccgctgtgtccaataccagtgaggatggcgagcttccatccttccagacattctcttgg	720
Qy	721	caccagcattagatgtccatccgtgggtctttaagcctcaccacaccttctcgtcttccatgg	780
Db	721	caccagcattagatgtccatccgtgggtctttaagcctcaccacaccttctcgtcttccatgg	780
Qy	781	ctggagctctatgtctgaaggccccacaatgaggtgggcactgcccacatgtatgtgacgc	840
Db	781	ctggagctctatgtctgaaggccccacaatgaggtgggcactgcccacatgtatgtgacgc	840
Qy	841	tggagtgagcacagagggcctggagctgcagtggtgtctggagctgtgtgtgggtaccctgg	900
Db	841	tggagtgagcacagagggcctggagctgcagtggtgtgtggagctgtgtgtgggtaccctgg	900
Qy	901	ttggactggggtgtgtggctgggtgcctcttgtaccaccgcccggggcaaggccctgg	960
Db	901	ttggactggggtgtgtggctgggtgcctcttgtaccaccgcccggggcaaggccctgg	960
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Db	961	aggagccagccaatgatatacaggaggatgccattgtctcccggaccctgcccctggccca	1020
Qy	1021	agagctcagacacaaatctccagaagaatgggacaccttctctgtcacctccgcacagagccc	1080
Db	1021	agagctcagacacaaatctccagaagaatgggacaccttctctgtcacctccgcacagagccc	1080
Qy	1081	tccggccaccctatggcctccaggcctgggtgcattgacccccacgccagctctctcca	1140
Db	1081	tccggccaccctatggcctccaggcctgggtgcattgacccccacgccagctctctcca	1140
Qy	1141	gccaggccctgcccaccagactgcccacgacagatgggggccaccctcaaccaatat	1200
Db	1141	gccaggccctgcccaccagactgcccacgacagatgggggccaccctcaaccaatat	1200
Qy	1201	cccccatccctgggtggggttcttctctggcttgagccgcattgggtgtgtgacctgtga	1260
Db	1201	cccccatccctgggtggggttcttctctggcttgagccgcattgggtgtgtgacctgtga	1260
Qy	1261	tgggtgcctgccagagtcgaagctggctctctggtatgatgacccccaccactcatggcta	1320
Db	1261	tgggtgcctgccagagtcgaagctggctctctggtatgatgacccccaccactcatggcta	1320
Qy	1321	aaggatttggggtctctccttccataaagggtcacctctagcacagaggcctgagtcctg	1380
Db	1321	aaggatttggggtctctccttccataaagggtcacctctagcacagaggcctgagtcctg	1380
Qy	1381	ggaaagagtcacactcctgaccccttagtactctgccccaccctctcttactgtgggaaa	1440
Db	1381	ggaaagagtcacactcctgaccccttagtactctgccccaccctctcttactgtgggaaa	1440
Qy	1441	accatctcagtaagacctaatgtgtccaggagacagaaggaggagtgatctctgga	1500
Db	1441	accatctcagtaagacctaatgtgtccaggagacagaaggaggagtgatctctgga	1500

### RESULT 3

AAA30052

ID AAA30052 standard; cDNA; 1813 BP.

AC AAA30052;

DT 09-AUG-2000 (first entry)

DE Human PRO246 nucleotide sequence.

Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261;  
PRO246;

KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;  
KW cell growth; proliferation; cell surface virus receptor; ADEPT;  
KW antibody dependent enzyme mediated prodrug therapy; ss.

OS Homo sapiens.

PN WO200015666-A2.

PD 23-MAR-2000.

08-SEP-1999; 99WO-US20594.

PR 10-SEP-1998: 98US-0099803.

XXXXXX

PA (GETH ) GENENTECH INC.

PI Goddard A, Gurney AL, Hillan KJ, Roy MA,<sup>\*</sup> Wood WI, Botstein D;

DR WPI: 2000-271386/23.

DR P-PSDB: AAY88574:

PT diagnosis and treatment of neoplastic cell growth and proliferation -  
XX Example 8; Fig 15; 200pp; English.

CC This sequence represents a human PRO246 nucleotide sequence. PRO246 is  
CC probably a cell surface virus receptor. The invention relates to  
isolated

CC antibodies which bind to a polypeptide. The "PRO" polypeptides are  
CC encoded by genes which are over expressed in the genome of tumour cells.  
CC Vectors and host cells comprising the nucleic acid encoding the  
CC antibodies are used in the production of the antibodies. The antibodies  
CC and nucleic acids encoding them are used for diagnosing a tumour in a  
CC mammal. The antibodies are used for inhibiting the growth of tumour  
cells

CC and identifying compounds that inhibit a biological or immunological  
CC activity of and/or expression of a PRO187, PRO533, PRO214, PRO240,  
CC PRO211, PRO230, PRO261, PRO246 or PRO317 polypeptide. The antibody can

be  
CC used in antibody dependent enzyme mediated prodrug therapy (ADAPT) by  
CC conjugating the antibody to a prodrug-activating enzyme which converts

a  
CC prodrug to an anti-cancer drug. The antibodies can be fluorescently  
CC labelled and monitored by light microscopy, flow cytometry or  
fluorimetry  
CC for diagnosis and prognosis of tumours.

XX  
SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 21; Length 1813;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps  
0;

QY 1 ggagccgacctgggtgcagcgctcggtcccgccagcgtccggtcgagcgt 60  
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DB 1 ggagccgacctgggtgcagcgctcggtcccgccagcgtccggtcgagcgt 60  
|||||

QY 61 cggcaacctgcaggtccgtcccgccgctggcgccctgactccgtcccgccagggga 120  
|||||

DB 61 cggcaacctgcaggtccgtcccgccgctggcgccctgactccgtcccgccagggga 120  
|||||

QY 121 gggccatgatttcctcccgggggccctgggtgaccaacttgctggtttttgttcctgg 180  
|||||

DB 121 gggccatgatttcctcccgggggccctgggtgaccaacttgctggtttttgttcctgg 180  
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QY 181 ggtgagtgccctcgccccctcccgccctcgggcccgctgcaactgcaactgcccccaacc 240  
|||||

DB 181 ggtgagtgccctcgccccctcccgccctcgggcccgctgcaactgcaactgcccccaacc 240  
|||||

QY 241 ggttcagcggtgagggagggggaagtgggtccctccagcgtggtacacctgcaacgggg 300  
|||||

DB 241 ggttcagcggtgagggagggggaagtgggtccctccagcgtggtacacctgcaacgggg 300  
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QY 301 aggtgtcttcatccagcgcctggaggtgccccctttgtgattggttcttcaaacagaaag 360  
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QY 361 aaaaggaggtatcaggtgtgtctctacatcaaatgggggtcacacaagcaaacctggaggtat 420  
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DB 361 aaaaggaggtatcaggtgtgtctctacatcaaatgggggtcacacaagcaaacctggaggtat 420  
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QY 781 ctggagctctatgtctgcaaggccccacaatgaggtgggctgcccactgccaatgtgacgc 840  
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|||||

DB 1141 gccaggccctgccccaccagactgccccacagatggggggccccaccctcaaccaatat 1200  
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Db	1741	taaaactaacatgaatatgtgtgttttctatttgcaaatattaaataacacataatg	1800	PR 18-FEB-2000; 2000WO-US04341.
Qy	1801	tttgtatgaaaaa 1813		PR 18-FEB-2000; 2000WO-US04342.
Db	1801	tttgtatgaaaaa 1813		PR 22-FEB-2000; 2000WO-US04414.
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ID	AAS21412	standard; cDNA; 1813 BP.		PR 01-MAR-2000; 2000WO-US05601.
XX	AC	AAS21412;		PR 20-MAR-2000; 2000WO-US07377.
XX	DT	24-OCT-2001 (first entry)		PR 21-MAR-2000; 2000WO-US07532.
XX	DE	Human cDNA sequence encoding for PRO246 polypeptide.		PR 30-MAR-2000; 2000WO-US08439.
XX	KW	Human secretory and transmembrane; PRO; mammalian; cancer; lung;		PR 17-MAY-2000; 2000WO-US13705.
KW	KW	breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;		PR 22-MAY-2000; 2000WO-US14042.
KW	KW	cartilage; ear; proliferation; glucose; free fatty acid; skeletal		PR 30-MAY-2000; 2000WO-US14941.
				PR 02-JUN-2000; 2000WO-US15264.
				PR 10-NOV-2000; 2000WO-US30873.
				XX (GETH ) GENENTECH INC.
				PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
				XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
				PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
				XX WFI; 2001-408281/43.
				DR P-PSDB; AAU12340.
				XX Isolated, secretory and transmembrane PRO polypeptide used to detect
				PT other PRO polypeptides, link bioactive molecules to cells expressing
				PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
				PT lung, breast, prostate, cervical
				XX Claim 3; Fig 337; 813pp; English.
				PS AAS21244-AAS21518 encode for novel human secretory and transmembrane
				XX PRO polypeptides. The PRO polypeptides are useful to detect other
				CC PRO polypeptides, to link bioactive molecules to cells expressing

PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.

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Query Match      .. 100.0%; Score 1813; DB 22; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

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 ID AAF60372 standard; cDNA; 1813 BP.  
 XX  
 AC AAF60372;  
 XX  
 DT 27-APR-2001 (first entry)  
 XX  
 DE PRO246 coding sequence.  
 XX  
 KW Cytostatic; PRO protein; tumour; cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200105836-A1.  
 XX  
 PD 25-JAN-2001.  
 XX  
 XX 20-DEC-1999; 99WO-US30999.  
 PF  
 XX 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 08-SEP-1999; 99WO-US20594.

13-SEP-1999; 99WO-US20944.  
 15-SEP-1999; 99WO-US21090.  
 05-OCT-1999; 99WO-US23089.  
 29-NOV-1999; 99WO-US28214.  
 30-NOV-1999; 99WO-US28313.  
 02-DEC-1999; 99WO-US28564.

(GETH ) GENENTECH INC.  
 Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;  
 WPI; 2001-091968/10.  
 P-PSDB; AAB68599.

New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,  
 useful for diagnosing and treating cancers -

Claim 50; Fig 15; 196pp; English.

The present invention relates to PRO proteins and coding sequences. The  
 present sequence is the coding sequence for one such PRO protein.  
 It was found that the PRO genes are amplified in the genome of tumour  
 cells. The gene amplification is expected to be associated with the  
 overexpression of the gene product and contributes to tumorigenesis.  
 Therefore, antagonists of PRO proteins are useful for the treatment of  
 benign or malignant tumours, leukaemias, lymphoid malignancies and other  
 disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,  
 epithelial, inflammatory and immunologic disorders.

Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 22; Length 1813;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps  
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Qy 1 ggagcgccttggtgtcagcggctcggtcccgccagcagctccggtcgccgagcct 60  
 Db 1 ggagcgccttggtgtcagcggctcggtcccgccagcagctccggtcgccgagcct 60  
 Qy 61 cggcactgcaggtcggtcggtcccgccggtcggtcccgccagcagcctcggtccgagcagc 120  
 Db 61 cggcactgcaggtcggtcggtcccgccggtcggtcccgccagcagcctcggtccgagcagc 120  
 Qy 121 gggccatgatttccctcccgcccgcccgcccgcccgcccgcccgcccgcccgcccgcccgcc 180  
 Db 121 gggccatgatttccctcccgcccgcccgcccgcccgcccgcccgcccgcccgcccgcccgcc 180  
 Qy 181 ggctgagtgccctcgcccgcccgcccgcccgcccgcccgcccgcccgcccgcccgcccgcc 240  
 Db 181 ggctgagtgccctcgcccgcccgcccgcccgcccgcccgcccgcccgcccgcccgcccgcc 240  
 Qy 241 ggttgaggcgggtggaggaggaggaggaggaggaggaggaggaggaggaggaggaggaggagg 300  
 Db 241 ggttgaggcgggtggaggaggaggaggaggaggaggaggaggaggaggaggaggaggaggagg 300  
 Qy 301 aggtgtcttcatccagccatggagggtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 360

Db	1201	cccccatccctgggtggggttcttctcctggcttgagccgcattgggtgctgctgctga	1260
Qy	1261	tggtgctgccagagactcaagctggctctctgggtatgatgacccaccacactcattggcta	1320
Db	1261	tggtgctgccagagactcaagctggctctctgggtatgatgacccaccacactcattggcta	1320
Qy	1321	aaggatttggggtctctccttctctataaagggtcacctctagcacagagcctgagtcag	1380
Db	1321	aaggatttggggtctctccttctctataaagggtcacctctagcacagagcctgagtcag	1380
Qy	1381	ggaagagtcacactcctgacccttagtactctgccccccacctctcttactgtgggaaa	1440
Db	1381	ggaagagtcacactcctgacccttagtactctgccccccacctctcttactgtgggaaa	1440
Qy	1441	accatctcagtaagacctaagtgtccaggagacagaaggagaagtggaatctctgga	1500
Db	1441	accatctcagtaagacctaagtgtccaggagacagaaggagaagtggaatctctgga	1500
Qy	1501	attgggaggagcctccaccacccctgactcctcttatgaagccagctgctgaaattag	1560
Db	1501	attgggaggagcctccaccacccctgactcctcttatgaagccagctgctgaaattag	1560
Qy	1561	ctactcaccagagtgagggggagagacttccagtcactgagtcctccaggcccccttga	1620
Db	1561	ctactcaccagagtgagggggagagacttccagtcactgagtcctccaggcccccttga	1620
Qy	1621	tctgtacccccaccctatctaacaccacccttggtctccactccagctccctgtattgat	1680
Db	1621	tctgtacccccaccctatctaacaccacccttggtctccactccagctccctgtattgat	1680
Qy	1681	ataacctgtcaggtggttggttagtttactggggcagagagatagggaatctcttat	1740
Db	1681	ataacctgtcaggtggttggttagtttactggggcagagagatagggaatctcttat	1740
Qy	1741	taaaactaacatgaatatgtgtgttttcatttgcaaatatttaataaagatacataatg	1800
Db	1741	taaaactaacatgaatatgtgtgttttcatttgcaaatatttaataaagatacataatg	1800
Qy	1801	tttgtatgaaaaa	1813
Db	1801	tttgtatgaaaaa	1813
RESULT 6			
AAC87040			
ID	AAC87040 standard; cDNA; 1813 BP.		
XX			
AC	AAC87040;		
XX			
DT	20-APR-2001 (first entry)		
XX			
DE	Nucleotide sequence of human polypeptide PRO246.		
XX			
KW	Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;		
KW	PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361;		
KW	PRO1308;		

## RESULT 6

AAC87040

ID AAC87040 standard: CDNA: 1813.BP.




























AAC87040;

XX

DT 20-APR-2001 (first entry)















































































































































DE Nucleotide sequence of human polypeptide PR0246.

•

KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;

KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361;

PRO1308;

PS	PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318; PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356; PRO346; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630; PRO6309; cell death; genetic disorder; transgenic animal; gene therapy; ss.	XX	Claim 2; Fig 57; 244pp; English.		
OS	Homo sapiens.	XX	The present sequence encodes a human secreted and transmembrane polypeptide. The specification describes human polypeptides, designated PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288, PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170, PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187, PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003, PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells can be modulated with agents that bind to these polypeptides, resulting in the death of the cells. The polynucleotides encoding these polypeptides are useful in the recombinant production of the polypeptides, as a hybridisation probe to screen libraries to isolate homologous sequences, or to map the gene. They may also be used for analysing genetic disorders, and to produce transgenic animals which are useful for the development and screening of therapeutically useful reagents. The polynucleotides can also be used in gene therapy e.g. to replace a defective gene.	XX	
PD	21-DEC-2000.	XX	SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;		
PP	22-MAY-2000; 2000WO-US14042.	XX			
XX	15-JUN-1999; 99US-0139695.	PR	Query Match 100.0%; Score 1813; DB 22; Length 1813;		
PR	20-JUL-1999; 99US-0145070.	PR	Best Local Similarity 100.0%; Pred. No. 0;		
PR	26-JUL-1999; 99US-0145698.	PR	Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
PR	17-AUG-1999; 99US-0149396.	PR			
PR	01-SEP-1999; 99WO-US20111.	PR			
PR	08-SEP-1999; 99WO-US20594.	PR			
PR	15-SEP-1999; 99WO-US21090.	PR			
PR	15-SEP-1999; 99WO-US21547.	PR			
PR	30-NOV-1999; 99WO-US28313.	PR			
PR	01-DEC-1999; 99WO-US28301.	PR			
PR	02-DEC-1999; 99WO-US28565.	PR			
PR	07-DEC-1999; 99US-0169495.	PR			
PR	05-JAN-2000; 2000WO-US00219.	PR			
PR	18-FEB-2000; 2000WO-US04341.	PR			
PR	18-FEB-2000; 2000WO-US04342.	PR			
PR	22-FEB-2000; 2000WO-US04414.	PR			
PR	01-MAR-2000; 2000WO-US05601.	PR			
PR	02-MAR-2000; 2000WO-US05841.	PR			
PR	20-MAR-2000; 2000WO-US07377.	PR			
PR	30-MAR-2000; 2000WO-US08439.	PR			
PR	15-MAY-2000; 2000WO-US13358.	PR			
PR	17-MAY-2000; 2000WO-US13705.	PR			
XX	(GETH ) GENENTECH INC.	XX			
PA	Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL; Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J; Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM; Wood WI, Zhang Z;	XX			
XX	WPI; 2001-050091/06..	XX			
DR	P-PSDB; AAC87040.	XX			
XX	Isolated nucleic acid molecule encoding a PRO polypeptide which is a transmembrane polypeptide is useful for gene therapy and identification of related polypeptides -	XX			
PT		PT			
PT		PT			
XX		XX			



Pf		22-FEB-2000; 2000WO-US04414.			
Xx					
Pr		07-JUL-1999; 99US-0143048.			
Pr		26-JUL-1999; 99US-0145698.			
Pr		28-JUL-1999; 99US-0146222.			
Pr		08-SEP-1999; 99WO-US20594.			
Pr		13-SEP-1999; 99WO-US20944.			
Pr		15-SEP-1999; 99WO-US21090.			
Pr		15-SEP-1999; 99WO-US21547.			
Pr		05-OCT-1999; 99WO-US23089.			
Pr		29-NOV-1999; 99WO-US28214.			
Pr		30-NOV-1999; 99WO-US28313.			
Pr		16-DEC-1999; 99WO-US30095.			
Pr		20-DEC-1999; 99WO-US30911.			
Pr		20-DEC-1999; 99WO-US30999.			
Pr		05-JAN-2000; 99WO-US00219.			
Xx					
Pa	(GETH ) GENENTECH INC.				
Xx	Ashkenazi AJ, Botstein D, Deanoyers L, Eaton DL, Ferrara N;				
PI	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;				
PI	Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;				
PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;				
PI	Williams PM, Wood WT;				
Xx					
DR	WPI; 2001-081051/09.				
DR	P-PSDB; AAB80219.				
Xx					
PT	Sixty one nucleic acids encoding PRO polypeptides which are useful in				
PT	the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung				
PT	squamous cell carcinoma) and neurodegenerative diseases (e.g.				
PT	Alzheimer's disease) -				
Xx					
PS	Claim 2; Fig 16; 393pp; English.				
Xx					
CC	The present sequence is one of sixty one nucleic acids encoding novel				
CC	secreted and transmembrane PRO polypeptides. The PRO polypeptides are				
CC	useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung				
CC	squamous cell carcinoma), gastrointestinal disorders (e.g.				
CC	enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,				
CC	Parkinson's disease), wound repair, cardiovascular disorders (e.g.				
CC	endometrial bleeding angiogenesis, ischaemias such as coronary				
CC	ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,				
CC	rheumatoid arthritis, multiple sclerosis), infertility, AIDS and				
CC	diabetes and retinal disorders such as retinitis pigmentosum.				
CC	The PRO nucleic acids have applications in molecular biology, including				
CC	use as hybridization probes, and in chromosome and gene mapping.				
Xx					
SQ	Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;				
	Query Match	100.0%; Score 1813; DB 22; Length 1813;			
	Best Local Similarity	100.0%; Pred.No. 0;			
	Matches 1813; Conservative	0; Mismatches	0; Indels	0; Gaps	
O;					
Oy	1 ggagccgcccgttgtagcggctcggtccccgcacgctccggccgctcgcgagcctt				

Qy 961 agagccagccaatgatatacaaggaggatgccattgctccccggaccctgcccctgggccc 1020  
 Db 961 agagccagccaatgatatacaaggaggatgccattgctccccggaccctgcccctgggccc 1020  
 Qy 1021 agagctcagacacaatctccaagaatggacccttctctgtcacctccgcagagccc 1080  
 Db 1021 agagctcagacacaatctccaagaatggacccttctctgtcacctccgcagagccc 1080  
 Qy 1081 tccggccaccccatggccctccccaggcctgggtgattgacccccacgcccagctctctcca 1140  
 Db 1081 tccggccaccccatggccctccccaggcctgggtgattgacccccacgcccagctctctcca 1140  
 Qy 1141 gccaggccctgcccctcaccagaactgcccacgacagatggggccaccctcaaccaatat 1200  
 Db 1141 gccaggccctgcccctcaccagaactgcccacgacagatggggccaccctcaaccaatat 1200  
 Qy 1201 ccccatccctggtgggtttctctctggttgagcccgatgggtgctgctgtga 1260  
 Db 1201 ccccatccctggtgggtttctctctggttgagcccgatgggtgctgctgtga 1260  
 Qy 1261 tgggtcctgccagagtcaggctgctctggtgatgacccccaccactcatggcta 1320  
 Db 1261 tgggtcctgccagagtcaggctgctctggtgatgacccccaccactcatggcta 1320  
 Qy 1321 aaggatttgggtctctctctctataaagggtcacctctagcacagaggcctgagtcag 1380  
 Db 1321 aaggatttgggtctctctctctataaagggtcacctctagcacagaggcctgagtcag 1380  
 Qy 1381 ggaaagagtcacactcctgaccttagtactctgccccaccctctcttactgtggaaa 1440  
 Db 1381 ggaaagagtcacactcctgaccttagtactctgccccaccctctcttactgtggaaa 1440  
 Qy 1441 accatctcagtaagacctaagtgctccaggagacagaggaagtgatctgga 1500  
 Db 1441 accatctcagtaagacctaagtgctccaggagacagaggaagtgatctgga 1500  
 Qy 1501 attggaggagcctccaccaccctgactcctcttatgaagccagctgctgaaattag 1560  
 Db 1501 attggaggagcctccaccaccctgactcctcttatgaagccagctgctgaaattag 1560  
 Qy 1561 ctactcaccagagtgaggggcagagacttccagtcactgagctccaggcccccttga 1620  
 Db 1561 ctactcaccagagtgaggggcagagacttccagtcactgagctccaggcccccttga 1620  
 Qy 1621 tctgtacccccccctctatctaacacaccccttggtccccactccagctccctgtattgat 1680  
 Db 1621 tctgtacccccccctctatctaacacaccccttggtccccactccagctccctgtattgat 1680  
 Qy 1681 ataactgtcaggctggctgttagtttactggggcagagatagggaatctcttat 1740  
 Db 1681 ataactgtcaggctggctgttagtttactggggcagagatagggaatctcttat 1740  
 Qy 1741 taaaactaacatgaatatgtgtgttttctatttgcaaatatttaataaagatacataatg 1800  
 |||||||

Db 1801 ttgtatgaaaa 1813  
 |||||||

RESULT 8  
 AAC97441  
 ID AAC97441 standard; cDNA; 1813 BP.  
 XX  
 AC AAC97441;  
 XX  
 DT 28-FEB-2001 (first entry)  
 XX  
 DE Human angiogenesis-associated protein PRO246 cDNA, SEQ ID NO:95.  
 XX  
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
 KW gene therapy; transgenic animal; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200053753-A2.  
 PD 14-SEP-2000.  
 XX  
 PF 05-JAN-2000; 2000WO-US00219.  
 XX  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
 XX  
 DR WPI; 2001-090793/10.  
 DR P-PSDB; AAB53082.

XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX  
PS Claim 58; Fig 37; 293pp; English.  
XX  
CC The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising  
a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO  
proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a cDNA encoding a  
PRO  
CC protein of the invention.  
XX  
SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 22; Length 1813;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps  
0;  
Qy 1 ggagcgcctgggtgtcagcgggtcggtcccgacgacgtccggtcggtcgagcgt 60  
|||||  
Db 1 ggagcgcctgggtgtcagcgggtcggtcccgacgacgtccggtcggtcgagcgt 60  
|||||  
Qy 61 cggcactgcaggtcgtcggtcccggtcggtcccgactcgtcccggtcggtcgagcgt 120  
|||||  
Db 61 cggcactgcaggtcgtcggtcccggtcggtcccgactcgtcccggtcggtcgagcgt 120  
|||||

Qy 121 gggccatgatttcc 180  
|||||  
Db 121 gggccatgatttcc 180  
|||||  
Qy 181 ggctgagtcctcgc 240  
|||||  
Db 181 ggctgagtcctcgc 240  
|||||  
Qy 241 ggttcagggcgggtggagggagggggaagtgggtctccagcgtgggtacacctgacacgggg 300  
|||||  
Db 241 ggttcagggcgggtggagggagggggaagtgggtctccagcgtgggtacacctgacacgggg 300  
|||||  
Qy 301 aggtgtcttcatcccgagccatggggaggtgccccctttgtgatgtgggttttcaaacagaaaag 360  
|||||  
Db 301 aggtgtcttcatcccgagccatggggaggtgccccctttgtgatgtgggttttcaaacagaaaag 360  
|||||  
Qy 361 aaaagaggatcaggtgtgtctctacatcaatcgggtgacacaaagcaaacctggaggtat 420  
|||||  
Db 361 aaaagaggatcaggtgtgtctctacatcaatcgggtgacacaaagcaaacctggaggtat 420  
|||||  
Qy 421 ccttggtctactccatgcctcccggaacctgtccctgcggtggaggggtctccaggaga 480  
|||||  
Db 421 ccttggtctactccatgcctcccggaacctgtccctgcggtggaggggtctccaggaga 480  
|||||  
Qy 481 aagactggccctacagctgctccgtgaatgtgcaagacacaaagcaaacctcaggg 540  
|||||  
Db 481 aagactggccctacagctgctccgtgaatgtgcaagacacaaagcaaacctcaggg 540  
|||||  
Qy 541 gccacagcatcaaaaccttagaactcaatgtactggttctccagctccctccatcctgcc 600  
|||||  
Db 541 gccacagcatcaaaaccttagaactcaatgtactggttctccagctccctccatcctgcc 600  
|||||  
Qy 601 gtctccagggtgtgccccatgtgggggcaaacgtgacctggagctgcagctcccaaggga 660  
|||||  
Db 601 gtctccagggtgtgccccatgtgggggcaaacgtgacctggagctgcagctcccaaggga 660  
|||||  
Qy 661 gtaagcccgctgtccaataccagtgaggatgggagctccatcctccagactcttcttg 720  
|||||  
Db 661 gtaagcccgctgtccaataccagtgaggatgggagctccatcctccagactcttcttg 720  
|||||  
Qy 721 caccagcattagatgtcatcgtgggtcttttaagcctcaccacaccttcgtctccatgg 780  
|||||  
Db 721 caccagcattagatgtcatcgtgggtcttttaagcctcaccacaccttcgtctccatgg 780  
|||||  
Qy 781 ctggagtcctatgtctgcaaggccacaaatgaggtgggagctgcccaatgtaagtgcgc 840  
|||||  
Db 781 ctggagtcctatgtctgcaaggccacaaatgaggtgggagctgcccaatgtaagtgcgc 840  
|||||  
Qy 841 tggaaagtgcagcagggcctggagctgcagtggtgtgagctgtgtgggtaccctgg 900  
|||||  
Db 841 tggaaagtgcagcagggcctggagctgcagtggtgtgagctgtgtgggtaccctgg 900  
|||||  
Qy 901 ttggactgggtgtggtgggtggtcctctgtaccacggcggggcaagggccctgg 960  
|||||  
Db 901 ttggactgggtgtggtgggtggtcctctgtaccacggcggggcaagggccctgg 960  
|||||  
Qy 961 aggagccagcgaatgatcatcaaggaggatgccattgtccccggaccctgcctggccca 1020  
|||||

ID AAF93785 standard; cDNA; 1821 BP.  
XX  
AC AAF93785;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE Human cDNA encoding a membrane or secretory protein clone PSEC0086.  
XX  
KW Human; secretory protein; membrane protein; vaccine; gene therapy;  
rheumatoid arthritis; diabetes; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1067182-A2.  
XX  
PD 10-JAN-2001.  
XX  
PF 07-JUL-2000; 2000EP-0114090.  
XX  
PR 08-JUL-1999; 99JP-0194179.  
PR 11-JAN-2000; 2000JP-0118775.  
PR 02-MAY-2000; 2000JP-0183766.  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
XX  
DR WPI; 2001-093989/11.  
XX  
DR P-PSDB; AAB88358.  
XX  
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
gene therapy or as candidate target molecules in drug development -  
XX  
PS Claim 1; SEQ ID 83; 609pp + CD ROM; English.  
XX  
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916  
which encode human secretory or membrane proteins represented by  
AAB88317 - AAB88419. Included in the invention are primers  
AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate  
the  
CC cDNA sequences of the invention. The invention also includes methods for  
the production of antibodies directed against the proteins, and cDNA  
sequences, which can be used in vaccines. The polynucleotide sequences  
can be used in gene therapy. The polynucleotide sequences and the  
proteins they encode may be used in the prevention, treatment and  
diagnosis of diseases associated with inappropriate secretory  
protein/membrane protein expression. The nucleic acids and complementary  
sequences may also be used as DNA probes in diagnostic assays  
(e.g. polymerase chain reactions (PCR)) to detect and quantitate the  
presence of similar nucleic acid sequences in samples. They may also be  
used to study the expression and function of secretory proteins/membrane  
polypeptides and their role in metabolism. The polypeptides may be used  
as antigens in the production of antibodies against them and in assays  
to  
CC identify modulators (agonists and antagonists) of expression and  
activity. The antibodies and antagonists may also be used as therapeutic

QY 1021 agagctcagacacaatctccaagaatggagcccttctctgtcacctccgcacgagccc 1080  
|||  
Db 1021 agagctcagacacaatctccaagaatggagcccttctctgtcacctccgcacgagccc 1080  
|||  
QY 1081 tcgggccacccatggcctccagggctgggtgattgaccccccacgcccagctctcca 1140  
|||  
Db 1081 tcgggccacccatggcctccagggctgggtgattgaccccccacgcccagctctcca 1140  
|||  
QY 1141 gccaggccctgccctcaccaagactgccacgacagatggggcccccacccctcaaccaatat 1200  
|||  
Db 1141 gccaggccctgccctcaccaagactgccacgacagatggggcccccacccctcaaccaatat 1200  
|||  
QY 1201 ccccatccctgggggtttctctctctggcttgagccgcagctgggtgctgtgctgtga 1260  
|||  
Db 1201 ccccatccctgggggtttctctctctggcttgagccgcagctgggtgctgtgctgtga 1260  
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QY 1261 tgggtcctgccacagtcgaagctggctctctggtatgatgacccccaccactcattggcta 1320  
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Db 1441 accatctcagtaagacctgaagtgctccaggagacagaaggagaagtgatctgga 1500  
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QY 1501 attggaggagcctccaccaccctgactcctcttatgaagccagctgctgaaattag 1560  
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QY 1741 taaactaacatgaatatgtgtgttttctatttgcaaatatttaataaagatacataatg 1800  
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QY 1801 tttgtatgaaaaa 1813  
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Db 1801 tttgtatgaaaaa 1813  
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<b>Qy</b>	1561	ctactcaccaagagtgagggcagagacttccagtcactgagtcctcccaggcccccttga	1620
<b>Db</b>	1572	ctactcaccaagagtgagggcagagacttccagtcactgagtcctcccaggcccccttga	1631
<b>Qy</b>	1621	tctgtacccaccacctatctaaccaccaccttggtcccaactccagtcctcctgatatgat	1680
<b>Db</b>	1632	tctgtacccaccacctatctaaccaccaccttggtcccaactccagtcctcctgatatgat	1691

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Query Match      99.6%; Score 1806.6; DB 22; Length 1827;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1809; Conservative 0; Mismatches 4; Indels 0;
0;

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QY	1	ggagcgcgccctgggtgctcagcggtccggtccccgcgcacgctccggccgttcgcgacgacct	60
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QY	61	cggcacctgcaggctcogtgcgtccgcgggtggcgccttgactcogtccggccaggga	120
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QY	121	ggggccatgattccctcccggggccctggtgaccaacttgctggggttttgttctctgg	180
Dd	133	ggggccatgattccctcccggggccctggtgaccaacttgctggggttttgttctctgg	192
QY	181	ggctgagtgcctcgcgcgccctccgcggccagctgcaactgcaactgccccccaacc	240
Dd	193	ggctgagtgcctcgcgcgccctccgcggccagctgcaactgcaactgccccccaacc	252
QY	241	ggttgacaggcggtggaggggagggaagtggctccagcgtggtacaccttgacagggg	300
Dd	253	ggttgacaggcggtggaggggagggaagtggctccagcgtggtacaccttgacagggg	312
QY	301	agggtgtcttcaccccagccatgggagggtgccttttgtgatgtggtcttcaaacagaaag	360
Dd	313	agggtgtcttcaccccagccatgggagggtgccttttgtgatgtggtcttcaaacagaaag	372
QY	361	aaaaggaggatcagggtgtgtcctacatcaatggggtcacacaagcaaacctggagtat	420
Dd	373	aaaaggaggatcagggtgtgtcctacatcaatggggtcacacaagcaaacctggagtat	432
QY	421	ccttggtctactccatgcctcccggaaacctgtcctcgggctgggggtctccaggaga	480
Dd	433	ccttggtctactccatgcctcccggaaacctgtcctcgggctgggggtctccaggaga	492
QY	481	aagactctggcccctacagctgctccgtgaatgtcgaaagcaaacaggcctaactctagg	540
Dd	493	aagactctggcccctacagctgctccgtgaatgtcgaaagcaaacaggcctaactctagg	552
QY	541	gccacagcatcaaaaaccttagaactcaatgtactggttctccagctcctccatcctgcc	600
Dd	553	gccacagcatcaaaaaccttagaactcaatgtactggttctccagctcctccatcctgcc	612
QY	601	gtctccagggtgtgcctccatgtgggggcaaacgtgacctgagctgacctccaagga	660

RESULT 10  
AAH02949

ID AAH02949 standard: DNA: 1827 BP.

XX  
AC AAH03949;

DT 15-JUN-20

**X**

DE Human shear stress-response coding sequence SEQ ID NO: 143.

KW Human; shear stress-response protein; vascular disease;  
arteriosclerosis; ds.

OS Homo sapiens.

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PN WO200125427-A1.



PD 12-APR-2001.



PF 02-OCT-2000; 2000WO-JP06840.

PR 01-OCT-1999; 99JP-0280976.

• **XX**

PA (KYOW ) KYOWA HAKKO KOGYO KK

PA (NOJI/) NOJIMA H.



PI Nojima H, Yoshisue H, Obayashi M, Ota T

PI Kuga T, Sekine S, Nakamura Y, Sugano S;

XX

DR WPI; 2001-266308/

DR P-PSDB; AAB90818.

XX DNA sequences, proteins encoded by them and antibodies against them  
PT useful in diagnosis and treatment of vascular disease caused by  
PT arteriosclerosis -

39

PD 12-JUL-2001.

XX 28-DEC-2000; 2000WO-JP09359.

PF 06-JAN-2000; 2000JP-0000585.

XX 06-JAN-2000; 2000JP-0000588.

PR 11-JAN-2000; 2000JP-0002299.

PR 03-FEB-2000; 2000JP-0026862.

PR 03-MAR-2000; 2000JP-0058367.

XX (PROT-) PROTEGENE INC.

PA (SAGA ) SAGAMI CHEM RES CENT.

XX Kato S, Kimura T;

PI WPI; 2001-418355/44.

XX P-PSDB; AAE06610.

DR Human proteins with hydrophobic domains and the nucleic acids encoding

XX them, useful for preventing diagnosing and treating e.g. cancer,

PT Alzheimer's and inflammation -

PS Claim 4; Page 486-489; 563pp; English.

XX The present sequence is human protein with hydrophobic domain encoding

CC cDNA clone HP10801. The polynucleotide and polypeptide of the invention

CC may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate polypeptide expression. The

CC polynucleotides

CC may be used to produce the polypeptide, by inserting the nucleic acids

CC into a host cell and culturing the cell to express the protein. The

CC polynucleotides and its complementary sequences may also be used as DNA

CC probes in diagnostic assays and also used in gene therapy. The

CC polypeptides may also be used as antigens in the production of

CC antibodies

CC and in assays to identify modulators of polypeptide expression and

CC activity. The polypeptides and nucleic acids may be used as nutritional

CC supplements, to modulate cytokine and cell proliferation activity, to

CC modulate immune stimulation or suppression (e.g. for the treatment of

CC microbial infections and autoimmune disorders such as multiple

CC sclerosis,

CC rheumatoid arthritis and insulin-dependent diabetes), to modulate

CC haematopoiesis, to modulate tissue growth activity (e.g. for the

CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's

CC disease), to modulate activin and inhibin activity (e.g. for controlling

CC fertility), to modulate chemotactic and chemokinetic activity, to

CC modulate haemostatic and thrombolytic activity, to modulate receptor

CC ligand activity, to modulate inflammation and to inhibit tumour growth.

XX

SQ Sequence 1816 BP; 362 A; 560 C; 488 G; 406 T; 0 other;

Query Match 99.5%; Score 1804.8; DB 22; Length 1816;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1806; Conservative 0; Mismatches 2; Indels 0; Gaps

0;

Qy 1741 taaaactaaacgaatcatgtgctgtctccatcttgcgaatttcaataaagatacataatg 1808  
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 Db 1749 taaaactaaacgaatcatgtgctgtctccatcttgcgaatttcaataaagatacataatg 1808  
 Qy 1801 ttgtgtatg 1808  
 ||||||||  
 Db 1809 ttgtgtatg 1816  
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 RESULT 12  
 AAA23441  
 ID AAA23441 standard; cDNA; 1954 BP.  
 XX  
 AC AAA23441;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE cDNA encoding human secreted protein vc5l\_1, SEQ ID NO:37.  
 KW Human; secreted protein; cancer; tumour; cardiovascular disorder;  
 KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;  
 KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;  
 KW neurodegenerative disease; asthma; contraceptive; ss.  
 XX Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 139..1311  
 FT /\*tag= a  
 FT /product= "Human secreted protein vc5l\_1"  
 XX  
 PN WO200011015-A1.  
 XX 02-MAR-2000.  
 XX 24-AUG-1998; 98US-0097638.  
 XX 24-AUG-1998; 98US-0097659.  
 XX 09-SEP-1998; 98US-0099618.  
 XX 28-SEP-1998; 98US-0102092.  
 XX 25-NOV-1998; 98US-0109978.  
 XX 23-DEC-1998; 98US-0113645.  
 XX 23-DEC-1998; 98US-0113646.  
 XX 23-AUG-1999; 99US-0379246.  
 XX (ALPH-) ALPHAGENE INC.  
 PA Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;  
 XX  
 DR WPI; 2000-224657/19.  
 DR P-PSDB; AAY94999.  
 XX  
 PT New secreted or transmembrane proteins and polynucleotides encoding  
 PT them, useful for treating neurodegenerative disorders, autoimmune  
 PT diseases and cancer -  
 XX  
 PS Claim 46; Page 296; 357pp; English.

360 gaaaggaggaatcagggtgtgtctctacatcaatgggggtcacaagcaaacctcggagta 419  
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373 gaaaggaggaatcagggtgtgtctctacatcaatgggggtcacaagcaaacctcggagta 432  
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420 tcccttgatctactccatgcctccgggaacctgtccctcggctggagggtctccaggag 479

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493	bb	aaagactctggccctcacagtgtccctgtaatgtgcaagacaaacaaaggcaaatctagg	552
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553	bb	ggccacagcatcaaaccttagaactcaatgtactgggtcctccagctcctccatcctgc	612
600	2y	cgtctccagggtgtgccccatgtg999ggcaaacgtgacctgagctgcagctctccaagg	659
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660	2y	agtaagcccgctgtccaataccagtggggtcggcagcttccatccttccagacttcttt	719
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[illegible]

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[illegible]

**1100**

1140 agccaggccctgcctaccacgaagactgccccacagatggggcccccacctcaaccaata 1199

Db 1153 agccaggccctgccctcaccaagactgccacgacagatggggccaccctcaaccaata 1212

| Accession | Gene | Protein               | Species           | Length | Weight | PI   | Inst. | Pub. | Ref. |
|-----------|------|-----------------------|-------------------|--------|--------|------|-------|------|------|
| U00001    | act  | actin                 | Homo sapiens      | 418    | 42022  | 5.27 | EMBL  | 1981 | 1    |
| U00002    | adp  | adenosine diphosphate | Homo sapiens      | 246    | 24600  | 4.75 | EMBL  | 1981 | 1    |
| U00003    | afp  | alpha-fetoprotein     | Homo sapiens      | 695    | 72720  | 5.5  | EMBL  | 1981 | 1    |
| U00004    | alb  | albumin               | Homo sapiens      | 585    | 66020  | 5.1  | EMBL  | 1981 | 1    |
| U00005    | act  | actin                 | Canis familiaris  | 418    | 42022  | 5.27 | EMBL  | 1981 | 1    |
| U00006    | adp  | adenosine diphosphate | Canis familiaris  | 246    | 24600  | 4.75 | EMBL  | 1981 | 1    |
| U00007    | afp  | alpha-fetoprotein     | Canis familiaris  | 695    | 72720  | 5.5  | EMBL  | 1981 | 1    |
| U00008    | alb  | albumin               | Canis familiaris  | 585    | 66020  | 5.1  | EMBL  | 1981 | 1    |
| U00009    | act  | actin                 | Rattus norvegicus | 418    | 42022  | 5.27 | EMBL  | 1981 | 1    |
| U00010    | adp  | adenosine diphosphate | Rattus norvegicus | 246    | 24600  | 4.75 | EMBL  | 1981 | 1    |
| U00011    | afp  | alpha-fetoprotein     | Rattus norvegicus | 695    | 72720  | 5.5  | EMBL  | 1981 | 1    |
| U00012    | alb  | albumin               | Rattus norvegicus | 585    | 66020  | 5.1  | EMBL  | 1981 | 1    |
| U00013    | act  | actin                 | Equus caballus    | 418    | 42022  | 5.27 | EMBL  | 1981 | 1    |
| U00014    | adp  | adenosine diphosphate | Equus caballus    | 246    | 24600  | 4.75 | EMBL  | 1981 | 1    |
| U00015    | afp  | alpha-fetoprotein     | Equus caballus    | 695    | 72720  | 5.5  | EMBL  | 1981 | 1    |
| U00016    | alb  | albumin               | Equus caballus    | 585    | 66020  | 5.1  | EMBL  | 1981 | 1    |
| U00017    | act  | actin                 | Bos taurus        | 418    | 42022  | 5.27 | EMBL  | 1981 | 1    |
| U00018    | adp  | adenosine diphosphate | Bos taurus        | 246    | 24600  | 4.75 | EMBL  | 1981 | 1    |
| U00019    | afp  | alpha-fetoprotein     | Bos taurus        | 695    | 72720  | 5.5  | EMBL  | 1981 | 1    |
| U00020    | alb  | albumin               | Bos taurus        | 585    | 66020  | 5.1  | EMBL  | 1981 | 1    |
| U00021    | act  | actin                 | Ovis montanus     | 418    | 42022  | 5.27 | EMBL  | 1981 | 1    |
| U00022    | adp  | adenosine diphosphate | Ovis montanus     | 246    | 24600  | 4.75 | EMBL  | 1981 | 1    |
| U00023    | afp  | alpha-fetoprotein     | Ovis montanus     | 695    | 72720  | 5.5  | EMBL  | 1981 | 1    |
| U00024    | alb  | albumin               | Ovis montanus     | 585    | 66020  | 5.1  | EMBL  | 1981 | 1    |
| U00025    | act  | actin                 | Lepus timidus     | 418    | 42022  | 5.27 | EMBL  | 1981 | 1    |
| U00026    | adp  | adenosine diphosphate | Lepus timidus     | 246    | 24600  | 4.75 | EMBL  | 1981 | 1    |
| U00027    | afp  | alpha-fetoprotein     | Lepus timidus     | 695    | 72720  | 5.5  | EMBL  | 1981 | 1    |
| U00028    | alb  | albumin               | Lepus timidus     | 585    | 66020  | 5.1  | EMBL  | 1981 | 1    |
| U00029    | act  | actin                 | Canis lupus       | 418    | 42022  | 5.27 | EMBL  | 1981 | 1    |
| U00030    | adp  | adenosine diphosphate | Canis lupus       | 246    | 24600  | 4.75 | EMBL  | 1981 | 1    |
| U00031    | afp  | alpha-fetoprotein     | Canis lupus       | 695    | 72720  | 5.5  | EMBL  | 1981 | 1    |
| U00032    | alb  | albumin               | Canis lupus       | 585    | 66020  | 5.1  | EMBL  | 1981 | 1    |
| U00033    | act  | actin                 | Canis lupus       | 418    | 42022  | 5.27 | EMBL  | 1981 | 1    |
| U00034    | adp  | adenosine diphosphate | Canis lupus       | 246    | 24600  | 4.75 | EMBL  | 1981 | 1    |
| U00035    | afp  | alpha-fetoprotein     | Canis lupus       | 695    | 72720  | 5.5  | EMBL  | 1981 | 1    |
| U00036    | alb  | albumin               | Canis lupus       | 585    | 66020  | 5.1  | EMBL  | 1981 | 1    |
| U00037    | act  | actin                 | Canis lupus       | 418    | 42022  | 5.27 | EMBL  | 1981 | 1    |
| U00038    | adp  | adenosine diphosphate | Canis lupus       | 246    | 24600  | 4.75 | EMBL  | 1981 | 1    |
| U00039    | afp  | alpha-fetoprotein     | Canis lupus       | 695    | 72720  | 5.5  | EMBL  | 1981 | 1    |
| U00040    | alb  | albumin               | Canis lupus       | 585    | 66020  | 5.1  | EMBL  |      |      |

CC secreted proteins.

XX

SQ Sequence 1932 BP; 405 A; 585 C; 514 G; 424 T; 4 other;

Query Match 98.4%; Score 1783.8; DB 21; Length 1932;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1804; Conservative 3; Mismatches 1; Indels 2; Gaps

2;

QY 4 gcgcgcctgggtgcagcggctcggctccgcgcacgtccgcgcctcggccgtgcgcagcctcgg 63  
|||||  
DB 9 gcgcgcctgggtgcagcggctcggctccgcgcacgtccgcgcctcggccgtgcgcagcctcgg 67  
|||||  
QY 64 cactgcaggtcgtgcgtccgcgcgtggcgcctgactcgtccgcgcagggaggg 123  
|||||  
DB 68 cactgcaggtcgtgcgtccgcgcgtggcgcctgactcgtccgcgcagggaggg 127  
|||||  
QY 124 ccatgattccctccgcgcgcctggcgcacaaactgctgcgtttttgttctcgggc 183  
|||||  
DB 128 ccatgattccctccgcgcgcctggcgcacaaactgctgcgtttttgttctcgggc 187  
|||||  
QY 184 tgagtgcctcgcgcgcctccgcgcgcctgcgcgcagctgcaactgcaactgcccgcacacggct 243  
|||||  
DB 188 tgagtgcctcgcgcgcctccgcgcgcctgcgcgcagctgcaactgcaactgcccgcacacggct 247  
|||||  
QY 244 tgcagcgggtggagggagggaagtgggtgtccagcgtgggtacaccttgacacctggcaggggagg 303  
|||||  
DB 248 tgcagcgggtggagggagggaagtgggtgtccagcgtgggtacaccttgacacctggcaggggagg 307  
|||||  
QY 304 tgtcttcacccagccatgggaggtgccttttgcgtggtgttcttcaaacagaaagaaa 363  
|||||  
DB 308 tgtcttcacccagccatgggaggtgccttttgcgtggtgttcttcaaacagaaagaaa 367  
|||||  
QY 364 agaggatcaggtgtgtctacatcaatgggggtcacacaagaacacctggagtatcct 423  
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DB 368 agaggatcaggtgtgtctacatcaatgggggtcacacaagaacacctggagtatcct 427  
|||||  
QY 424 tggctactccatgcctccgcgcgcctgtccctggcgtggaggggtctccagggagaaag 483  
|||||  
DB 428 tggctactccatgcctccgcgcgcctgtccctggcgtggaggggtctccagggagaaag 487  
|||||  
QY 484 actctggccctacagctgctccgtgaatgtgcaagacaacaaaggcaaatcaggggccc 543  
|||||  
DB 488 actctggccctacagctgctccgtgaatgtgcaagacaacaaaggcaaatcaggggccc 547  
|||||  
QY 544 acagatcaaaaccttagaactcaatgactggttctcctccagctcctccatcctgccgtc 603  
|||||  
DB 548 acagatcaaaaccttagaactcaatgactggttctcctccagctcctccatcctgccgtc 607  
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QY 604 tccaggggtgtgcccctgtggggggcaaacgtgacctgagctgacctgacctcccaaggagta 663  
|||||  
DB 608 tccaggggtgtgcccctgtggggggcaaacgtgacctgagctgacctgacctcccaaggagta 667  
|||||  
QY 664 agcccgctgtccaataaccagtgggatcggcagcttccatcctccagacttcttggcac 723  
|||||  
DB 668 agcccgctgtccaataaccagtgggatcggcagcttccatcctccagacttcttggcac 727  
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DB 728 cagcattagatgtcatcgtgggtctttaagcctaccaaccttctcgtctccatggctg 787  
|||||  
QY 784 gagtctatgtctgcagggcccaaatgaggtgggcaactgcccccaatgtaatgtgacgctgg 843  
|||||  
DB 788 gagtctatgtctgcagggcccaaatgaggtgggcaactg-ccaatgtaatgtgacgctgg 846  
|||||  
QY 844 aagtgcagcacagggcctggagctgcagtggttctgctggagctggttgggtacctcgggttg 903  
|||||  
DB 847 aagtgcagcacagggcctggagctgcagtggttctgctggagctggttgggtacctcgggttg 906  
|||||  
QY 904 gactggggtgtcgtgggtgggtcgtctctgtaccacgcgcgggggcaaggccctcggagg 963  
|||||  
DB 907 gactggggtgtcgtgggtgggtcgtctctgtaccacgcgcgggggcaaggccctcggagg 966  
|||||  
QY 964 agccagccaatgatatacaaggagatgccattgctccccgggacactgcccctggcccaaga 1023  
|||||  
DB 967 agccagccaatgatatacaaggagatgccattgctccccgggacactgcccctggcccaaga 1026  
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QY 1024 gctcagacacaatcctcaagaatggggaccccttctcctgtcacctccgcagagccctcc 1083  
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DB 1027 gctcagacacaatcctcaagaatggggaccccttctcctgtcacctccgcagagccctcc 1086  
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QY 1084 ggccaccccatggcctccagggcctgtgcatgaccccccagccagctctctccagcc 1143  
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DB 1087 ggccaccccatggcctccagggcctgtgcatgaccccccagccagctctctccagcc 1146  
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QY 1144 aggcctgcctcaccagaactgcccacgacagatggggccacacccctcaaccaatctcc 1203  
|||||  
DB 1147 aggcctgcctcaccagaactgcccacgacagatggggccacacccctcaaccaatctcc 1206  
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QY 1204 ccacccctgggtgggttctcctcctggtgagccgcatggggtgctgctgctgctgagtg 1263  
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DB 1207 ccacccctgggtgggttctcctcctggtgagccgcatggggtgctgctgctgctgagtg 1266  
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QY 1264 tgcctgcccagagtcgaagctgggtcctctggtatgatgaccccccacactcattggctaaag 1323  
|||||  
DB 1267 tgcctgcccagagtcgaagctgggtcctctggtatgatgaccccccacactcattggctaaag 1326  
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QY 1324 gatttggggtctctcctcctataaagggtcacctctagcacagagccctgagtcagtgga 1383  
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DB 1327 gatttggggtctctcctcctataagggtcacctctagcacagagccctgagtcagtgga 1386  
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QY 1384 aagagtcacactcctgaccccttagtactctgccccccacactccttcttactgtgggaaacc 1443  
|||||  
DB 1387 aagagtcacactcctgaccccttagtactctgccccccacactccttcttactgtgggaaacc 1446  
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QY 1444 atctcagtaagacctaaagtgtccaggagacagaagagaagagtgagtcctcggaaatt 1503  
|||||  
DB 1447 atctcagtaagacctaaagtgtccaggagacagaagagaagagtgagtcctcggaaatt 1506  
|||||  
QY 1504 gggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattagcta 1563  
|||||  
DB 1507 gggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattagcta 1566  
|||||  
QY 1564 ctccacaaagagtgaggggcagagactccagtcactgagctccagggccccccttgatct 1623  
|||||

CC and polypeptides encoded by the genes. Expression vectors and host cells  
CC for producing the polypeptides are disclosed and methods for screening  
or  
CC purifying ligands which specifically bind to the polypeptides are also  
CC provided. The polynucleotides are useful for treating diseases  
associated  
CC with the altered expression of a gene that is coexpressed with one or  
CC more known atherosclerosis-associated genes in a subject. They are  
CC useful in diagnosis, prognosis, treatment, prevention, selection and  
CC evaluation of therapies for atherosclerosis including stroke, myocardial  
CC infarction, transient cerebral ischemia, mesenteric ischemia, coronary  
CC artery disease, angina pectoris, peripheral vascular disease, renal  
CC artery stenosis, and hypertension. Sequences AAC85065-85098 represent  
CC atherosclerosis-associated genes of the invention.  
xx  
SQ Sequence 1831 BP; 370 A; 561 C; 494 G; 406 T; 0 other;

Query Match 97.1%; Score 1760.4; DB 22; Length 1831;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 1807; Conservative 0; Mismatches 6; Indels 13;

|    |     |                                                                |     |
|----|-----|----------------------------------------------------------------|-----|
| QY | 1   | ggagcgccttgggtgtcagcgctcggtcccgcgcaagctcgggccgttcgcgcaagcct    | 60  |
|    |     |                                                                |     |
| Db | 3   | ggagcgccttgggtgtcagcggtcggtcccgcgcaagctcgggccgttcgcgcaactc     | 62  |
|    |     |                                                                |     |
| QY | 61  | cggcacctgcaggatccgt-gcgtcccggcct-ggcgccctgaactccgtccccgcacgg   | 118 |
|    |     |                                                                |     |
| Db | 63  | gggcacctgcaggatccgtggcgctcccgcggtggcgccctgaactccgtccccgcacgg   | 122 |
|    |     |                                                                |     |
| QY | 119 | gagggccaatgatattccctcccggggccctggtagaccaacttgctgcgggttttgttcct | 178 |
|    |     |                                                                |     |
| Db | 123 | gagggccaatgatattccctcccggggccctggtagaccaacttgctgcgggttttgttcct | 182 |
|    |     |                                                                |     |
| QY | 179 | ggggctgagtgccctcgcgccccctcggggccagctgcaactgcacattgccgcgcaa     | 238 |
|    |     |                                                                |     |
| Db | 183 | ggggctgagtgccctcgcgccccctcggggccagctgcaactgcacattgccgcgcaa     | 242 |
|    |     |                                                                |     |
| QY | 239 | ccggttcaggcggtggaggaggaaagtgggtgttccagcgtggtacaccttgcaagg      | 298 |
|    |     |                                                                |     |
| Db | 243 | ccggttcaggcggtggaggaggaaagtgggtgttccagcgtggtacaccttgcaagg      | 302 |
|    |     |                                                                |     |
| QY | 299 | ggaggtgtcttcattcccagccatgggagggtgcccttttgtgatgtggttctcaaacagaa | 358 |
|    |     |                                                                |     |
| Db | 303 | ggaggtgtcttcattcccagccatgggagggtgcccttttgtgatgtggttctcaaacagaa | 362 |
|    |     |                                                                |     |
| QY | 359 | agaaaaggaggatcaggtgtgtcctacatacaatgggggtcacaagaagcaaacctggaagt | 418 |
|    |     |                                                                |     |
| Db | 363 | agaaaaggaggatcaggtgtgtcctacatacaatgggggtcacaagaagcaaacctggaagt | 422 |
|    |     |                                                                |     |
| QY | 419 | atccttgggtactcccatgccctccgggaacctgtccctgcggtcgaggggtctccagga   | 478 |
|    |     |                                                                |     |
| Db | 423 | atccttgggtactcccatgccctccgggaacctgtccctgcggtcgaggggtctccagga   | 482 |
|    |     |                                                                |     |
| QY | 479 | gaaagacttggcccctaagctgctccgtgaatgtgcagacacaaaggcaaatctag       | 538 |
|    |     |                                                                |     |
| Db | 483 | gaaagacttggcccctaagctgctccgtgaatgtgcagacacaaaggcaaatctag       | 542 |
|    |     |                                                                |     |

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|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|----------------------------------------------------------------|------|
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1567 | ctcaccaagagtgaggggcagagacttcagtcactgagctctccaggcccccttgatct    | 1626 |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1624 | gtacccacccttatctaacaccacccttggtccccactccagctccctgtattgatata    | 1683 |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1627 | gtacccacccttatctaacaccacccttggtccccactccagctccctgtattgatata    | 1686 |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1684 | acctgtcaggctggcttggttgaggttttactggggcagaggataggggaatctcttattaa | 1743 |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1687 | acctgtcaggctggcttggttgaggttttactggggcagaggataggggaatctcttattaa | 1746 |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1744 | aactaacatgaatatgtgtgttttcatttgcaaatattaaataagatacatataatgttt   | 1803 |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1747 | aactaacatgaatatgtgtgttttcatttgcaaatattaaataagatacatataatgttt   | 1806 |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1804 | gatatgaaaaa                                                    | 1813 |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1807 | gatatgaaaaa                                                    | 1816 |
| <p>RESULT 14</p> <p>AAC85076</p> <p>ID AAC85076 standard; DNA; 1831 BP.</p> <p>XX</p> <p>AC AAC85076;</p> <p>XX</p> <p>DT 08-MAY-2001 (first entry)</p> <p>XX</p> <p>DE Atherosclerosis-associated gene seq ID No. 12.</p> <p>XX</p> <p>KW Atherosclerosis-associated gene; stroke; myocardial infarction; human; ischemia; coronary artery disease; angina pectoris; hypertension; peripheral vascular disease; renal artery stenosis; antiatherosclerotic; cerebroprotective; cardiant; gene therapy; hypotensive; vasotropic; antianginal; ds.</p> <p>XX</p> <p>OS Homo sapiens.</p> <p>XX</p> <p>PN WO200104264-A2.</p> <p>XX</p> <p>PD 18-JAN-2001.</p> <p>XX</p> <p>PF 28-JUN-2000; 2000WO-US17887.</p> <p>XX</p> <p>PR 07-JUL-1999; 99US-0349015.</p> <p>XX</p> <p>PA (INCY-) INCYTE GENOMICS INC.</p> <p>XX</p> <p>PI Jones KA, Volkmuth W, Walker MG;</p> <p>XX</p> <p>DR WPI; 2001-138330/14.</p> <p>XX</p> <p>PT Composition comprising atherosclerosis-associated polynucleotide useful in diagnosis, prognosis, treatment, and prevention of atherosclerosis and stroke, myocardial infarction, or hypertension -</p> <p>XX</p> <p>PS Claim 1; Page 43; 58pp; English.</p> <p>XX</p> <p>CC The invention provides novel atherosclerosis-associated polynucleotides</p> |      |                                                                |      |

RESULT 15  
AAF44978  
ID AAF44978 standard; cDNA; 1869 BP.  
XX  
AC AAF44978;  
XX  
DT 28-MAR-2001 (first entry)  
XX  
DE Human INTERCEPT 258 coding sequence SEQ ID NO: 26.

AA44978  
ID A44978 standard; CDNA; 1869 BP.  
XX  
XX  
XX A44978;  
XX AC  
XX AC  
XX  
DT 28-MAR-2001 (first entry)  
XX  
XX  
DE Human INTERCEPT 258 coding sequence SEQ ID NO: 26.

Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281; INTERCEPT 258; coronary disorder; olfactory disorder; neurological disorder; pulmonary disorder; immunological disorder; developmental disorder; kidney disorder; ss.

WO200078808-A1.

19-JUN-2000; 2000WO-US16883.

18-JUN-1999: 99US-0336536.

(MILLER) MILLER PHARM INC.

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~~5: all~~

XX  
...cyclic acids for treating diseases, obesity, multiple  
...action, autoimmune diseases, arthritis, diabetes,  
WPI: 2001-050109/06.  
...diseases and disorders.

XX New nucleic acids, infect  
PT atherosclerosis, infect  
PT disorders, brain disor  
PT disorders, asthma

disorders, and asthma -  
sclerosis and asthma -  
English.

English:

PT sclerosis 1980; 10: 100-102. English.

Claim 1; 125-  
PS provides the prote-  
transmembrane proteins  
treatment of

XX The present invention  
XX The present invention  
XX The present invention

human and ma-  
cept 258. These

257, -TANGO 281 and INTERCEP-  
257, -TANGO 281 and INTERCEP-

coronary, 2.1 and kidney disorders, 1.08 T; 6 other;

developmental and

|    |             |             |    |
|----|-------------|-------------|----|
| XX | Length 1869 | BP: 391     | xx |
|    | 22:         | Length 1869 |    |

| Sequence | DB            | Gaps |
|----------|---------------|------|
| SQ       | score 1757.6; | 2;   |

|       | pred. | No. 0; | Indels |
|-------|-------|--------|--------|
| 96.9% |       | 22;    |        |
| 96.7% |       |        |        |

| Query Match | Similarity | Mismatch |
|-------------|------------|----------|
| 98.76%      | 0          | 0        |

Best Local  
Conservation  
1791:

Matches

z;

1 99agctctcagcggctcggctccctc  
QY -tgaactccgctcccgccagggg

28 ggagcgccctggg-  
28 ggcacggctggcgccctgg-  
28 ggcacggctggcgccaggga

bp  
-ccacctgcagggtccgtagcggccccc-  
-taccagccccctgactcgatcccca-

61 cggcac-----  
67 -----tccgtgcgtcccgaggctgga  
qy

|||||cggcactgcaggcccg-  
88 cggcactgcaggcccg-  
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-ccccctggtgaccaactgctg-

Db  
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-ccaaactgntgcggtttctgc

121 gggccacc-  
121 gggccaccctggtgaccac-  
-cacttgcccgcacaac

118 gggccatgatttcccccccccc

**db**

148 50-

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tccactgcactgcccccc

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181 ggctgagctgc  
181 ggctgagctgc

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208:55-  
db  
db

241 ggttcgaggcggcttgcagcaac

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-+atgatgtggtcttcaag

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268 ggccgcg  
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- - - |||||  
- - - |||||

ccatccagcctgggagg  
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[illegible][illegible]

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 Qy 1799 tgttgtatgaaaa 1813  
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 Db 1828 tgttgtatgagata 1842  
 |||||

Search completed: August 19, 2002, 16:16:06  
 Job time: 4314 sec

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:02:47 ; Search time 54.72 Seconds  
(without alignments)  
8138.405 Million cell updates/sec

Title: US-09-902-759-38  
Perfect score: 1813  
Sequence: 1 ggagccgctgggtgtcag.....cataatgtttgtatgaaaaa 1813

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq: \*  
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5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length  | ID | Description                          |
|------------|-------|-------------|---------|----|--------------------------------------|
| 1          | 1376  | 75.9        | 1387    | 2  | US-08-979-424-2 Sequence 2, Appli    |
| 2          | 51.4  | 2.8         | 7218    | 1  | US-08-232-463-14 Sequence 14, Appli  |
| 3          | 45.4  | 2.5         | 1584    | 4  | US-08-928-383B-1 Sequence 1, Appli   |
| 4          | 45.4  | 2.5         | 2434    | 4  | US-09-272-496-1 Sequence 1, Appli    |
| 5          | 44.2  | 2.4         | 4403765 | 4  | US-09-103-840A-2 Sequence 2, Appli   |
| 6          | 43.4  | 2.4         | 4403765 | 4  | US-09-103-840A-2 Sequence 2, Appli   |
| 7          | 42.4  | 2.3         | 1095    | 4  | US-08-928-383B-3 Sequence 3, Appli   |
| 8          | 42.2  | 2.3         | 2830    | 1  | US-07-882-292-1 Sequence 1, Appli    |
| 9          | 42.2  | 2.3         | 2830    | 2  | US-08-331-644-1 Sequence 1, Appli    |
| 10         | 42.2  | 2.3         | 2830    | 5  | PCT-US93-04102-1 Sequence 1, Appli   |
| 11         | 41.8  | 2.3         | 477     | 4  | US-09-135-994-1 Sequence 1, Appli    |
| 12         | 41.6  | 2.3         | 1515    | 4  | US-08-928-383B-25 Sequence 25, Appli |

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|------|------|-----|--------|---|-------------------|--------------------|
| C 13 | 41.2 | 2.3 | 1480   | 4 | US-09-000-130-4   | Sequence 7, Appli  |
| 14   | 41   | 2.3 | 441529 | 4 | US-09-103-840A-1  | Sequence 1, Appli  |
| 15   | 40.4 | 2.2 | 1355   | 3 | US-08-415-655-14  | Sequence 14, Appli |
| C 16 | 37.8 | 2.1 | 2576   | 1 | US-08-471-033-35  | Sequence 35, Appli |
| C 17 | 37.8 | 2.1 | 2576   | 2 | US-08-471-044-35  | Sequence 35, Appli |
| C 18 | 37.8 | 2.1 | 2576   | 2 | US-08-463-483A-35 | Sequence 35, Appli |
| C 19 | 37.8 | 2.1 | 2576   | 2 | US-08-471-046A-35 | Sequence 35, Appli |
| C 20 | 37.8 | 2.1 | 2576   | 2 | US-08-470-568B-35 | Sequence 35, Appli |
| C 21 | 37.8 | 2.1 | 2576   | 2 | US-08-469-334-35  | Sequence 35, Appli |
| C 22 | 37.8 | 2.1 | 2576   | 3 | US-09-300-529-35  | Sequence 35, Appli |
| C 23 | 37.8 | 2.1 | 2655   | 1 | US-08-471-033-17  | Sequence 17, Appli |
| C 24 | 37.8 | 2.1 | 2655   | 1 | US-08-471-033-26  | Sequence 26, Appli |
| C 25 | 37.8 | 2.1 | 2655   | 2 | US-08-471-044-17  | Sequence 17, Appli |
| C 26 | 37.8 | 2.1 | 2655   | 2 | US-08-471-044-26  | Sequence 26, Appli |
| C 27 | 37.8 | 2.1 | 2655   | 2 | US-08-463-483A-17 | Sequence 17, Appli |
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| C 30 | 37.8 | 2.1 | 2655   | 2 | US-08-471-046A-26 | Sequence 26, Appli |
| C 31 | 37.8 | 2.1 | 2655   | 2 | US-08-470-568B-17 | Sequence 17, Appli |
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| C 33 | 37.8 | 2.1 | 2655   | 2 | US-08-469-334-17  | Sequence 17, Appli |
| C 34 | 37.8 | 2.1 | 2655   | 2 | US-08-469-334-26  | Sequence 26, Appli |
| C 35 | 37.8 | 2.1 | 2655   | 3 | US-09-300-529-17  | Sequence 17, Appli |
| C 36 | 37.8 | 2.1 | 2655   | 3 | US-09-300-529-26  | Sequence 26, Appli |
| C 37 | 37.8 | 2.1 | 4031   | 1 | US-08-471-033-49  | Sequence 49, Appli |
| C 38 | 37.8 | 2.1 | 4031   | 2 | US-08-471-044-49  | Sequence 49, Appli |
| C 39 | 37.8 | 2.1 | 4031   | 2 | US-08-463-483A-49 | Sequence 49, Appli |
| C 40 | 37.8 | 2.1 | 4031   | 2 | US-08-471-046A-49 | Sequence 49, Appli |
| C 41 | 37.8 | 2.1 | 4031   | 2 | US-08-470-568B-49 | Sequence 49, Appli |
| C 42 | 37.8 | 2.1 | 4031   | 2 | US-08-469-334-49  | Sequence 49, Appli |
| C 43 | 37.8 | 2.1 | 4031   | 3 | US-09-300-529-49  | Sequence 49, Appli |
| C 44 | 37.4 | 2.1 | 320    | 4 | US-09-165-264-7   | Sequence 7, Appli  |
| C 45 | 37   | 2.0 | 1682   | 4 | US-09-318-443-7   | Sequence 7, Appli  |

ALIGNMENTS

RESULT 1  
US-08-979-424-2  
; Sequence 2, Application US/08979424  
; Patent No. 5942606  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS

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421 ccttggtctactccatgccctccggaaacctgtccctggctggagggctctccaggaga 480
420 CCTTGGTCTACTCCATGCCCTCCGGAACTGTCCCTGGGCTGGAGGGTCTCCAGGAGA 479
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480 AAGACTCTGGCCCTTACAGCTGCTCCGTGAATGTGCAAGACAAACAAAGGCAAACTTAGG 539
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,424
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0405 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGFET03
; CLONE: 1232054
; US-08-979-424-2

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Query Match 75.9%; Score 1376; DB 2; Length 1387;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1387; Conservative 0; Mismatches 0; Indels 1; Gaps
1;
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QY 61 cggcacctgcaggtccgtgctgcgcggcgtgcccctgactccgtcccgccagggga 120
Db 60 CGGCACCTGCAGGTCCTGCTGCCGCGGTGGCGCCCTGACTCCGTCCCGCGCAGGGA 119
QY 121 gggccatgatttccctccggggggccctgggtgaccaaactgtcgggtttttgttccctgg 180
Db 120 GGGCCATGATTTCCCTCCCGGGGCCCTGGTGACCAACTGTGCGGGTTTTGTCTCTGG 179
QY 181 ggtgagtgccctcgccccccctcgcgggcccaagctgcaactgcaactgcccccaacc 240
Db 180 GGCTGAGTGCCCTCGCGCCCTCCGCGGCCAGCTGCAACTGCACTTGCCCGCCCAACC 239
QY 241 ggttcgagcggtgagggagggaggtggtgcttccagcgtggtacacctgacagggg 300
Db 240 GGTTCAGCGGTGAGGGAGGGAAGTGTGCTTCCAGCGTGTGTACACTTGTGACGGGG 299
QY 301 aggtgtcttcatccagccatggagggtgcccccttctgtgattgtggttcttcaacagaaa 360
Db 300 AGGTGTCTTCATCCAGGCCATGGAGGTGCCCTTTGTGTGATGTGTTCTTCAACAGAAAG 359
QY 361 aaaaggaggatcaggtgtgtcctacatcaatggggtcacaaagcaaacctggagat 420

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|                                                  |      |                                                             |                                               |      |
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|                                                  |      |                                                             |                                               |      |
| Db                                               | 1260 | TGGTGCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCACCACTCATTGGCTA  | 1319                                          |      |
|                                                  |      |                                                             |                                               |      |
| Qy                                               | 1321 | aaggattgggtctctcctctctataaagggtcacctctagcacagagcctgagtcag   | 1380                                          |      |
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| Db                                               | 1320 | AAGGATTGGGTCTCTCTCTTCTATAAGGGTCACCTCTAGCACAGAGGCGCTGAGTCATG | 1379                                          |      |
|                                                  |      |                                                             |                                               |      |
| Qy                                               | 1381 | ggaaagag                                                    | 1388                                          |      |
|                                                  |      |                                                             |                                               |      |
| Db                                               | 1380 | GGAAAGAG                                                    | 1387                                          |      |
|                                                  |      |                                                             |                                               |      |
| RESULT 2                                         |      |                                                             |                                               |      |
| US-08-232-463-14                                 |      |                                                             |                                               |      |
| ; Sequence 14, Application US/08232463           |      |                                                             |                                               |      |
| ; Patent No. 5670367                             |      |                                                             |                                               |      |
| ; GENERAL INFORMATION:                           |      |                                                             |                                               |      |
| ; APPLICANT: DORNER, F.                          |      |                                                             |                                               |      |
| ; APPLICANT: SCHEIFLINGER, F.                    |      |                                                             |                                               |      |
| ; APPLICANT: FALKNER, F. G.                      |      |                                                             |                                               |      |
| ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  |      |                                                             |                                               |      |
| ; NUMBER OF SEQUENCES: 52                        |      |                                                             |                                               |      |
| ; CORRESPONDENCE ADDRESS:                        |      |                                                             |                                               |      |
| ; ADDRESSEE: Foley & Lardner                     |      |                                                             |                                               |      |
| ; STREET: 1800 Diagonal Road, Suite 500          |      |                                                             |                                               |      |
| ; CITY: Alexandria                               |      |                                                             |                                               |      |
| ; STATE: VA                                      |      |                                                             |                                               |      |
| ; COUNTRY: USA                                   |      |                                                             |                                               |      |
| ; ZIP: 22313-0299                                |      |                                                             |                                               |      |
| ; COMPUTER READABLE FORM:                        |      |                                                             |                                               |      |
| ; MEDIUM TYPE: Floppy disk                       |      |                                                             |                                               |      |
| ; COMPUTER: IBM PC compatible                    |      |                                                             |                                               |      |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS                |      |                                                             |                                               |      |
| ; SOFTWARE: PatentIn Release #1.0, Version #1.25 |      |                                                             |                                               |      |
| ; CURRENT APPLICATION DATA:                      |      |                                                             |                                               |      |
| ; APPLICATION NUMBER: US/08/232,463              |      |                                                             |                                               |      |
| ; FILING DATE:                                   |      |                                                             |                                               |      |
| ; CLASSIFICATION: 435                            |      |                                                             |                                               |      |
| ; PRIOR APPLICATION DATA:                        |      |                                                             |                                               |      |
| ; APPLICATION NUMBER: US/07/935,313              |      |                                                             |                                               |      |
| ; FILING DATE:                                   |      |                                                             |                                               |      |
| ; APPLICATION NUMBER: EP 91 114 300.6            |      |                                                             |                                               |      |

NAME: BENT, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703)836-9300  
 TELEFAX: (703)683-4109  
 TELEX: 899149  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7218 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:00:57 ; Search time 1589.67 Seconds  
(without alignments)  
15393.119 Million cell updates/sec

Title: US-09-902-759-38  
Perfect score: 1813  
Sequence: 1 ggagcgccctgggtgtcag.....cataatgtttgtatgaaaaa 1813

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: em\_esthum.\*  
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4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_htc.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_htc.\*  
12: gb\_gss.\*  
13: em\_gss\_hum.\*  
14: em\_gss\_inv.\*  
15: em\_gss\_pln.\*  
16: em\_gss\_vrt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score  | Match | Length | DB | ID       | Description       |
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|        | 2   | 1005.6 | 55.5  | 1017   | 9  | AL547358 | AL547358 AL547358 |

|           |       |      |      |    |          |                   |
|-----------|-------|------|------|----|----------|-------------------|
| 5         | 947.6 | 52.3 | 1013 | 9  | AL550211 | AL550211 AL550211 |
| 6         | 942.6 | 52.0 | 1003 | 9  | AL552901 | AL552901 AL552901 |
| C 7       | 942   | 52.0 | 955  | 9  | AL571713 | AL571713 AL571713 |
| C 8       | 937.2 | 51.7 | 1026 | 9  | AL573957 | AL573957 AL573957 |
| 9         | 911.6 | 50.3 | 969  | 9  | AL548482 | AL548482 AL548482 |
| 10        | 911   | 50.2 | 1109 | 9  | AL549789 | AL549789 AL549789 |
| C 11      | 910.2 | 50.2 | 998  | 9  | AL572321 | AL572321 AL572321 |
| 12        | 906.6 | 50.0 | 973  | 9  | AL549049 | AL549049 AL549049 |
| C 13      | 896   | 49.4 | 978  | 9  | AL576327 | AL576327 AL576327 |
| 14        | 895.8 | 49.4 | 938  | 9  | AL546335 | AL546335 AL546335 |
| 15        | 895.8 | 49.4 | 999  | 9  | AL554790 | AL554790 AL554790 |
| C 16      | 893.6 | 49.3 | 938  | 9  | AL574910 | AL574910 AL574910 |
| C 17      | 890.6 | 49.1 | 999  | 9  | AL577433 | AL577433 AL577433 |
| 18        | 886.2 | 48.9 | 920  | 9  | AL553280 | AL553280 AL553280 |
| 19        | 883.6 | 48.7 | 946  | 9  | AL551281 | AL551281 AL551281 |
| 20        | 863.6 | 47.6 | 894  | 9  | AL537139 | AL537139 AL537139 |
| 21        | 843.6 | 46.5 | 1816 | 11 | AK009223 | AK009223 Mus      |
| muscu     |       |      |      |    |          |                   |
| 22        | 842.8 | 46.5 | 907  | 9  | AL549957 | AL549957 AL549957 |
| 23        | 842.4 | 46.5 | 1859 | 11 | BC019460 | BC019460 Mus      |
| muscu     |       |      |      |    |          |                   |
| 24        | 830.6 | 45.8 | 900  | 9  | AL550946 | AL550946 AL550946 |
| 25        | 819.4 | 45.2 | 853  | 10 | BI771838 | BI771838          |
| 603055231 |       |      |      |    |          |                   |
| 26        | 809.8 | 44.7 | 853  | 9  | AL555047 | AL555047 AL555047 |
| 27        | 806.8 | 44.5 | 834  | 10 | BI769077 | BI769077          |
| 603057054 |       |      |      |    |          |                   |
| 28        | 798   | 44.0 | 878  | 9  | AL549197 | AL549197 AL549197 |
| C 29      | 787.6 | 43.4 | 886  | 9  | AL550912 | AL550912 AL550912 |
| 30        | 784.8 | 43.3 | 790  | 9  | AL551438 | AL551438 AL551438 |
| 31        | 777   | 42.9 | 885  | 10 | BI767362 | BI767362          |
| 603057503 |       |      |      |    |          |                   |
| 32        | 766   | 42.3 | 789  | 10 | BI821049 | BI821049          |
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| C 33      | 764.4 | 42.2 | 795  | 9  | AL577654 | AL577654 AL577654 |
| 34        | 758.2 | 41.8 | 872  | 10 | BI819730 | BI819730          |
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| 35        | 737.8 | 40.7 | 754  | 10 | BI771884 | BI771884          |
| 603055290 |       |      |      |    |          |                   |
| 36        | 726.2 | 40.1 | 774  | 10 | BI916766 | BI916766          |
| 603178773 |       |      |      |    |          |                   |
| 37        | 723.6 | 39.9 | 735  | 9  | AL547289 | AL547289 AL547289 |
| 38        | 723.6 | 39.9 | 833  | 10 | BI759939 | BI759939          |
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| 39        | 718   | 39.6 | 905  | 10 | BI818810 | BI818810          |
| 603037664 |       |      |      |    |          |                   |
| C 40      | 710   | 39.2 | 739  | 9  | AL566674 | AL566674 AL566674 |
| 41        | 707.4 | 39.0 | 753  | 10 | BI772732 | BI772732          |
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| 42        | 703.8 | 38.8 | 760  | 10 | BG759963 | BG759963          |
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| 43        | 699.8 | 38.6 | 782  | 10 | BI909870 | BI909870          |
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| 44        | 690.4 | 38.1 | 748  | 10 | BG758052 | BG758052          |
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ALIGNMENTS

RESULT 1  
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LOCUS 16-FEB-2001  
DEFINITION AL573851 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CS0DI054YI01.3  
prime, mRNA sequence.  
ACCESSION AL573851  
VERSION AL573851.1 GI:12933489  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1069)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
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was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed by  
Life Technologies. Contact : Feng Liang Life Technologies,  
a division of Invitrogen 9800 Medical Center Drive  
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"  
BASE COUNT 248 a 269 c 327 g 224 t 1 others  
ORIGIN

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Best Local Similarity 99.5%; Pred. No. 2.7e-232;  
Matches 1050; Conservative 0; Mismatches 3; Indels 2; Gaps  
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 13-FEB-2001  
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 prime, mRNA sequence.  
 ACCESSION AL513572  
 VERSION AL513572.1 GI:12777066  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1045)  
 AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
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 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-stranded cDNA was digested with Not I and  
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
 vector. Library was normalized. Library was constructed by  
 Life Technologies. Contact : Feng Liang Life Technologies,  
 a division of Invitrogen 9800 Medical Center Drive  
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
 Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com"  
 BASE COUNT 196 a 304 c 302 g 229 t 14 others  
 ORIGIN

Query Match 54.7%; Score 992.4; DB 9; Length 1045;  
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|                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                  |                   |
|-----------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------|-------------------|
| Db                    | 899                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | GTTCGCTGGCTGGTCTCTTTACCAACCGCGGGCAAGGCCTTGAGGAGCCAGC             | 958               |
| Qy                    | 971                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | caatgatataagaggatgccattgctcccccggaccctgccttgccttgccccaaagactcaga | 1030              |
| Db                    | 959                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | MAATGAATWAAGAGGATGCCATTCTCCCCGAGACCCTGCCCTGGCCCCAAGAGCTCAGA      | 1018              |
| Qy                    | 1031                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | cacaatctccaagaatggaccctttt 1056                                  |                   |
| Db                    | 1019                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | AATAATYTCCAAGAAATGGGACCCTT 1044                                  |                   |
| RESULT                | 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                  |                   |
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| 16-FEB-2001           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                  |                   |
| DEFINITION            | AL573030 LTI_NFL006_PL2 Homo sapiens cDNA clone CSDDI014YD08 3 prime, mRNA sequence.                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                  |                   |
| ACCESSION             | AL573030                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                  |                   |
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| KEYWORDS              | EST.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                  |                   |
| SOURCE                | human.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                  |                   |
| ORGANISM              | Homo sapiens                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                  |                   |
|                       | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                  |                   |
| REFERENCE             | 1 (bases 1 to 986)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                  |                   |
| AUTHORS               | Ld.W.B., Gruber,C., Jesse,J. and Polayes,D.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                  |                   |
| TITLE                 | Full-length cDNA libraries and normalization                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                  |                   |
| JOURNAL               | Unpublished (2001)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                  |                   |
| COMMENT               | Contact: Genoscope<br>Genoscope - Centre National de Sequencage<br>BP 191 91006 EVRY cedex - France<br>Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.                                                                                                                                                                                                                                                                                                                                                                 |                                                                  |                   |
| FEATURES              | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                  |                   |
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| BASE COUNT            | 212 a 250 c 302 g 210 t 12 others                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                  |                   |
| ORIGIN                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                  |                   |
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| Best Local Similarity | 98.1%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Pred. No. 1.1e-213;                                              |                   |
| Matches 969;          | Conservative 9;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Mismatches 8;                                                    | Indels 2; Gaps    |

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 16-FEB-2001  
 DEFINITION AL550211 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CS0DI039YD07 5  
 prime, mRNA sequence.  
 ACCESSION AL550211  
 VERSION AL550211.1 GI:12886963  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1013)  
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 CONTACT: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
 Location/Qualifiers

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/organism="Homo sapiens"

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/clone="CS0DI039YD07"

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 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-stranded cDNA was digested with Not I and  
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
 vector. Library was normalized. Library was constructed by  
 Life Technologies. Contact : Feng Liang Life Technologies,  
 a division of Invitrogen 9800 Medical Center Drive  
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
 Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com"  
 BASE COUNT 183 a 309 c 304 g 216 t 1 others  
 ORIGIN

Query Match 52.3%; Score 947.6; DB 9; Length 1013;  
 Best Local Similarity 99.3%; Pred.No. 1.1e-213;  
 Matches 1003; Conservative 1; Mismatches 0; Indels 6; Gaps

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 Db 359 TCAGTGTGTTCTTACATCAATGGGTGTCACAAAGCAAACTGGAGTATCTTTGCTCTA 418  
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 Db 419 CTCCATGCCCTCCCGAACCTGTCTCCGTGAGGGTCTCCAGAGAAAGACTCTGG 478  
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 Db 599 TGTGCCCATGTGGGGGCAACGTGACCTCCAGCTGCCAGTCTCCAAGGAGTAAGCCCGC 658  
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# RESULT 6

AL552901 AL552901 1003 bp mRNA linear EST  
 LOCUS 16-FEB-2001

DEFINITION AL552901 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CS0D1071YE19 5  
 prime, mRNA sequence.

ACCESSION AL552901

VERSION AL552901.1 GI:12892228

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1003)

AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

## FEATURES

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enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com"

BASE COUNT 183 a 304 c 301 g 213 t 2 others

## ORIGIN

Query Match

Best Local Similarity 52.0%; Score 942.6; DB 9; Length 1003;

Matches 975; Conservative 1; Mismatches 0; Indels 3; Gaps

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 REFERENCE 1 (bases 1 to 955)  
 AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001).  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
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 cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
 vector. Library was normalized. Library was constructed by  
 Life Technologies. Contact : Peng Liang Life Technologies,  
 a division of Invitrogen 9800 Medical Center Drive  
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
 Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com"  
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 REFERENCE 1 (bases 1 to 969)  
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
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 vector. Library was normalized. Library was constructed by  
 Life Technologies. Contact : Feng Liang Life Technologies,  
 a division of Invitrogen 9800 Medical Center Drive  
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
 Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com"  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1109)  
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
  
FEATURES  
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vector. Library was normalized. Library was constructed by  
Life Technologies. Contact : Feng Liang Life Technologies,  
a division of Invitrogen 9800 Medical Center Drive  
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
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VERSION AL572321.1 GI:12930475
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 998)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
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REFERENCE 1 (bases 1 to 938)  
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
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was primed with a NotI-oligo(dT) primer. Five prime end  
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cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed by  
Life Technologies. Contact : Feng Liang Life Technologies,  
a division of Invitrogen 9800 Medical Center Drive  
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"  
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250 cggtagggaggagggaagtgtgtctccagcgtgtacaccttgacggggaggtgtctt 309  
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240 CGGTGAGGAGGGGGAAGTGTGTCTTCCAGCGTGTACACCTTGCACGGGGAGGTGTCTT 299  
|||||  
310 catccagccatgggaggtgcccctttgtgtgtgttcttcaaacagagaaaaagagg 369  
|||||  
300 CATCCAGCCATGGAGGTGCCCTTTGTGATGTGTGTTCTTCAACAGAAAGAAAGAGG 359  
|||||  
370 atcaggtgtgtctcatcaatcaatgggtgacaaagcaaaccttgagtagtatccttggct 429  
|||||  
360 ATCAGGTGTGTCTTACATCAATGGGTACAAACAGCAAACTGGAGTATCCTTGGTCT 419  
|||||  
430 actccatgcccctccgggaacctgtccctgcggtggaggtctccaggagaagactctg 489  
|||||  
420 ACTCCATGCCCTCCCGGAACCTGTCCCTCGCGCTGGAGGGTCTCCAGGAGAAAGACTCTG 479  
|||||  
490 gccctacagctgtccgtgaatgtgcaagacaaacaaaggcaaatctaggggccacagca 549  
|||||  
480 GCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAAGGCAAAATCTAGGGGCCACAGCA 539  
|||||  
550 tcaaaccttagaactcaatgtactgttccctccagctcctccatcctcgtcctccagg 609  
|||||  
540 TCAAAACCTTAGAACTCAATGTACTGTCTCTCCAGCTCCTCCATCTCTCCGCTCCAGG 599  
|||||  
610 gtgtgccccatgtgggggcaaacgtgacctgagctgccagctcccaaggagtaagcccg 669  
|||||  
600 GTGTGCCCATGTGGGGCAAAACGTGACCTTGAGCTGCCAGTCTCCAAGGAGTAAGCCCG 659  
|||||  
670 ctgtccaataccagtggtggatcggtgagcttccatccttccagacttcttgcaccagcat 729  
|||||  
660 CTGTCCAATACCAGTGGGATCGGCAGCTTCCATCTCTCCAGACTTCTTTCGACACGAT 719  
|||||  
730 tagatgtcatccgtgggtctttaagcctcaccacaccttctcgtctccatggctggagctc 789  
|||||  
720 TAGATGTCTATCCGTGGGTCTTTAAGCCTCACCACCTTTCGCTTCCATGGCTGGAGTCT 779  
|||||  
790 atgtctgaagccccacaatgaggtgggactgccccaatgtaatgtgacgctggaagtga 849  
|||||  
780 ATGTCTGAAGCCCAATGAGGTGGGCACTGCCCCAATGTAATGTGACGCTGGAAGTGA 839  
|||||  
850 gcacagggcctggagctgagtggtgtgctggagctgtgtgggtaccctgggtggactgg 909  
|||||  
840 GCACAGGGCCTGGAGCTGACGTGGTGTCTGTGAGCTGTGTGGGTA -CCTGGTTGGACTGG 898  
|||||



OM protein - protein search, using sw model

Run on: August 19, 2002, 16:13:17 ; Search time 57.91 Seconds  
(without alignments)

updates/sec 748.036 Million cell

Title: US-09-902-759-39

Perfect score: 2012

Sequence: 1 MISLPGPLVTLRLFLGL.....SRMGAVPMVPAQSQAGSLV 390

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_032802.\*  
1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

AA27096

ID AA27096 standard; Protein; 390 AA.

| Result No. | Score | Match | Length | DB ID | Description |
|------------|-------|-------|--------|-------|-------------|
|------------|-------|-------|--------|-------|-------------|

|    |        |       |     |    |                            |
|----|--------|-------|-----|----|----------------------------|
| 1  | 2012   | 100.0 | 390 | 20 | AA27096 Human viral recept |
| 2  | 2012   | 100.0 | 390 | 20 | AA27096 Amino acid sequenc |
| 3  | 2012   | 100.0 | 390 | 20 | AA27096 EGF-like homologue |
| 4  | 2012   | 100.0 | 390 | 21 | AA27096 Human PRO246 amino |
| 5  | 2012   | 100.0 | 390 | 21 | AA27096 Human secreted pro |
| 6  | 2012   | 100.0 | 390 | 22 | AA27096 Human PRO246 polyp |
| 7  | 2012   | 100.0 | 390 | 22 | AA27096 Human membrane or  |
| 8  | 2012   | 100.0 | 390 | 22 | AA27096 PRO246. Homo sapi  |
| 9  | 2012   | 100.0 | 390 | 22 | AA27096 Amino acid sequenc |
| 10 | 2012   | 100.0 | 390 | 22 | AA27096 Human PRO246 prote |
| 11 | 2012   | 100.0 | 390 | 22 | AA27096 Human angiogenesis |
| 12 | 2004   | 99.6  | 390 | 22 | AA27096 Human protein havi |
| 13 | 2004   | 99.6  | 390 | 22 | AA27096 Human shear stress |
| 14 | 2003   | 99.6  | 389 | 21 | AA27096 Fragment of human  |
| 15 | 1738.5 | 86.4  | 370 | 22 | AA27096 Human INTERCEPT 25 |
| 16 | 1736.5 | 86.3  | 370 | 22 | AA27096 Human secreted pro |
| 17 | 1734.5 | 86.2  | 370 | 22 | AA27096 Human secreted pro |
| 18 | 1734.5 | 86.2  | 370 | 22 | AA27096 Human secreted pro |
| 19 | 1734.5 | 86.2  | 370 | 22 | AA27096 Human secreted pro |
| 20 | 1601.5 | 79.6  | 341 | 22 | AA27096 Murine mature INTE |
| 21 | 1581   | 78.6  | 321 | 22 | AA27096 Human viral recept |
| 22 | 1581   | 78.6  | 321 | 22 | AA27096 Human polypeptide  |
| 23 | 1579   | 78.5  | 325 | 21 | AA27096 Human clone vc51_1 |
| 24 | 1399   | 69.5  | 394 | 22 | AA27096 Murine secreted pr |
| 25 | 1397   | 69.4  | 394 | 22 | AA27096 Murine INTERCEPT 2 |
| 26 | 1397   | 69.4  | 394 | 22 | AA27096 Murine secreted pr |
| 27 | 1394   | 69.3  | 394 | 22 | AA27096 Murine secreted pr |
| 28 | 1393   | 69.2  | 394 | 22 | AA27096 Murine secreted pr |
| 29 | 1331   | 66.2  | 365 | 22 | AA27096 Murine mature INTE |
| 30 | 1232   | 61.2  | 246 | 22 | AA27096 Murine INTERCEPT 2 |
| 31 | 1207   | 60.0  | 237 | 21 | AA27096 Human secreted pro |
| 32 | 1107   | 55.0  | 220 | 22 | AA27096 Human INTERCEPT 25 |
| 33 | 1095   | 54.4  | 217 | 22 | AA27096 Human INTERCEPT 25 |
| 34 | 1027   | 51.0  | 206 | 22 | AA27096 Human INTERCEPT 25 |
| 35 | 965.5  | 48.0  | 212 | 20 | AA27096 Human secreted pro |
| 36 | 890    | 44.2  | 177 | 22 | AA27096 Human INTERCEPT 25 |
| 37 | 833.5  | 41.4  | 249 | 22 | AA27096 Murine INTERCEPT 2 |
| 38 | 833    | 41.4  | 172 | 22 | AA27096 Human polypeptide  |
| 39 | 577    | 28.7  | 182 | 22 | AA27096 Mouse 10.3 kDa pro |
| 40 | 467.5  | 23.2  | 120 | 22 | AA27096 Murine INTERCEPT 2 |
| 41 | 436    | 21.7  | 127 | 21 | AA27096 Human clone vc51_1 |
| 42 | 400.5  | 19.9  | 99  | 22 | AA27096 Murine INTERCEPT 2 |
| 43 | 400    | 19.9  | 80  | 22 | AA27096 Murine INTERCEPT 2 |
| 44 | 367.5  | 18.3  | 426 | 22 | AA27096 Human cDNA SEQ ID  |
| 45 | 361.5  | 18.0  | 376 | 19 | AA27096 Mouse coxsackievir |

AC AAY27096;  
 XX  
 DT 18-OCT-1999 (first entry)  
 XX  
 DE Human viral receptor protein (ACVRP).  
 XX  
 KW Viral receptor protein; ACVRP; cancer; viral disorder; inflammation;  
 KW gene therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5942606-A.  
 XX  
 PD 24-AUG-1999.  
 XX  
 PF 24-NOV-1997; 97US-0979424.  
 XX  
 PR 24-NOV-1997; 97US-0979424.  
 XX  
 PA (INCY-) INCYTE PHARM INC.,  
 XX Corley NC, Lal P;  
 PI  
 XX WPI; 1999-493538/41.  
 DR  
 DR N-PSDB; AAX87000.  
 XX  
 PS Isolated and purified polynucleotide useful for treating or  
 PT preventing cancer, inflammation and viral disorders  
 PT  
 XX Claim 1; Fig 1A-D; 28pp; English.  
 XX  
 CC This represents a human viral receptor protein (ACVRP). The protein  
 CC can be expressed by standard recombinant methodology. ACVRP can be used  
 CC for treating and/or preventing cancer, a viral disorder or inflammation  
 CC through the administration of a vector expressing a polynucleotide which  
 CC is fully complementary to the present sequence. Polynucleotides encoding  
 CC ACVRP can be used for diagnostic purposes to quantitate ACVRP expression  
 CC in biopsied tissues and correlate expression with disease. They can be  
 CC used to distinguish between the absence, presence and excess expression  
 CC of ACVRP and to monitor levels during therapeutic intervention.  
 CC Hybridisation probes can be used for mapping the naturally occurring  
 CC genomic sequence and detect differences in the chromosomal location in  
 CC normal, carrier or affected individuals. ACVRP may be ligated to a  
 CC heterologous sequence to produce a fusion protein which can be used to  
 CC screen peptide libraries for inhibitors of ACVRP activity and to screen  
 CC for novel antiproteoal and antifungal therapeutics. The expression  
 CC vectors which encode ACVRP can be used to deliver nucleotide sequences  
 CC to targeted organ, tissue or cell populations and complementary  
 CC polynucleotides to treat conditions associated with overexpression of  
 CC ACVRP by blocking transcription of the mRNA, modulating ACVRP activity  
 CC or regulating the gene function.  
 XX  
 SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 20; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-143;

0;  
 QY 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGVVLPAWYTLHGEV 60  
 Db 1 mislpgplvtnllrflflglalappsraqqlhlpanrlqaveggevvlpawylhgev 60  
 QY 61 SSSQPWEVFMWFFKQKQKEDQVLSYINGVTTTKPGVSLVYSMPERNLSLRLEGLQEKD 120  
 Db 61 sssqpwevfmwffkqkqkqkdvlsyingvtttkpgvslvysmpernlsrlrieglqekd 120  
 QY 121 SGPYSCSVNVQDKQKGRGHSIKTLELNLVLPAPPSCRLQGVPHVGANVTLSQSPRSK 180  
 Db 121 sgpyscsvnvqdkgkgrghsiktlemnlpappscrlqgvphvganvtlscqsprsk 180  
 QY 181 PAVQYQWDRQLPSFQTFPAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACNVTL 240  
 Db 181 pavqyqwdrlpsfqtffapaldvirgslsltnlsssmagvycvckahnevgtacnvtle 240  
 QY 241 VSTGPGAAVAVGAVVGTLLVGLLGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300  
 Db 241 vstgpgaaavavavvgtllvglglaglvlllyhrrgkaleepandikedaiaprtlpwps 300  
 QY 301 SDTISKNGTSSVTSARALRPPHGPGRPGALTPPSLSSQALPSRLPTTDGAHPQPISP 360  
 Db 301 sdtiskngtssvtsaralrpphgpgrpgaltptpslsaqalpsrlpttdgahppqipsp 360  
 QY 361 IPGGVSSGLSRMGAVPMVPAQSQAGSLV 390  
 Db 361 ipggvssglstrmgavpmvpaqsgagslv 390

# RESULT 2

AAV13351  
 ID AAV13351 standard; Protein; 390 AA.  
 XX  
 AC AAV13351;  
 XX  
 DT 25-JUN-1999 (first entry)  
 XX  
 DE Amino acid sequence of protein PRO246.  
 XX  
 KW Secreted protein; transmembrane protein; human; enterocolitis;  
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;  
 KW congenital microvillus atrophy; skin disease; cell growth;  
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;  
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;  
 KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;  
 KW anti-thrombotic; wound healing; tissue repair.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9914328-A2.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 16-SEP-1998; 98WO-US19330.  
 XX

PT New isolated human genes and polypeptides used in, e.g. treatment of  
 PT gastrointestinal ulceration  
 XX  
 PS Claim 12; Fig 17; 320pp; English.  
 XX  
 CC AAY1344-403 represent secreted and transmembrane human proteins.  
 CC The cDNA sequences are obtained from cDNA libraries, prepared from  
 CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.  
 CC The encoded polypeptides have specific uses based on their homology to  
 CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders  
 CC associated with the preservation and maintenance of gastrointestinal  
 CC mucosa and the repair of acute and chronic mucosal lesions  
 CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal  
 CC ulceration and congenital microvillus atrophy), skin diseases associated  
 CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial  
 CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),  
 CC potent effects on cell growth and development, diseases related to  
 CC growth or survival of nerve cells including Parkinson's disease,  
 CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as  
 CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used  
 CC as a target for anti-tumor drugs. PRO533 may be used in the treatment  
 CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an  
 CC anti-thrombotic agent; PRO287 polypeptides and portions may have  
 CC therapeutic applications in wound healing and tissue repair; PRO317 can  
 CC be used for treating problems of the kidney, uterus, endometrium, blood  
 CC vessels, or related tissue, e.g. in the heart of genital tract.  
 XX  
 SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 20; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-143;  
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps  
 0;  
 QY 1 MISLPGPLVTLNLRFLFLGLSALAPPSPRAQLQLHLPANRLQAVEGGEVLPWYTLHGEV 60  
 Db 1 mislpgplvtnlrlflglalsalappspraqqlhlpnrlqaveggevlpawtylhgev 60  
 QY 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVSMPSRNLSRLGLEQKXD 120  
 Db 61 sssqpwevpfvmwffkqkekedqvlsyngvttskpgvslvsmprnlsrlglelqekd 120  
 QY 121 SQPYSCSVNVQDKQKSRGHSIKTLENLVLPAPPSCRELQGVPHVGANVTLSQSPRSK 180  
 Db 121 sqpyscsvnvqdkqksgsrghsiktlenlvppappscrlqgvphvganvtlscqsprsk 180  
 QY 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSNAGVYVCKAHNEVGTAQCNVTLE 240  
 Db 181 pavqyqwdrlpsfqtffapaldvirgslsltnlssnagvyvckahnevgtaqcnvtle 240  
 QY 241 VSTPGGAAGVAGAVGTLVGLGLAGLVLLYHRRGKALKEEPANDIKEDAIAPRTLWPWKS 300  
 Db 241 vstpggaavagavgtlvglglaglvlllyhrrgkaleepandikedaiaprtlpwpsk 300  
 QY 301 SDTISKNGTLSSVTSARALRPPHPPRGALFTPTSSSQALSPRLPTDGAHPQPTSP 360  
 Db 301 sdtiskngtlssvtsaralrpphpprgaltptpsasqalpsrpttdgahppqpsp 360

RR 25-NOV-1997; 97US-0066840.  
 PR 17-SEP-1997; 97US-0059113.  
 PR 17-SEP-1997; 97US-0059115.  
 PR 17-SEP-1997; 97US-0059117.  
 PR 17-SEP-1997; 97US-0059119.  
 PR 17-SEP-1997; 97US-0059121.  
 PR 17-SEP-1997; 97US-0059122.  
 PR 17-SEP-1997; 97US-0059184.  
 PR 18-SEP-1997; 97US-0059263.  
 PR 18-SEP-1997; 97US-0059266.  
 PR 15-OCT-1997; 97US-0062125.  
 PR 17-OCT-1997; 97US-0062285.  
 PR 17-OCT-1997; 97US-0062287.  
 PR 21-OCT-1997; 97US-0063486.  
 PR 24-OCT-1997; 97US-0062814.  
 PR 24-OCT-1997; 97US-0062816.  
 PR 24-OCT-1997; 97US-0063045.  
 PR 24-OCT-1997; 97US-0063120.  
 PR 24-OCT-1997; 97US-0063121.  
 PR 24-OCT-1997; 97US-0063127.  
 PR 24-OCT-1997; 97US-0063128.  
 PR 27-OCT-1997; 97US-0063329.  
 PR 27-OCT-1997; 97US-0063327.  
 PR 28-OCT-1997; 97US-0063541.  
 PR 28-OCT-1997; 97US-0063542.  
 PR 28-OCT-1997; 97US-0063544.  
 PR 28-OCT-1997; 97US-0063549.  
 PR 28-OCT-1997; 97US-0063550.  
 PR 28-OCT-1997; 97US-0063564.  
 PR 29-OCT-1997; 97US-0063435.  
 PR 29-OCT-1997; 97US-0063704.  
 PR 29-OCT-1997; 97US-0063732.  
 PR 29-OCT-1997; 97US-0063738.  
 PR 29-OCT-1997; 97US-0063734.  
 PR 29-OCT-1997; 97US-0064215.  
 PR 29-OCT-1997; 97US-0063735.  
 PR 31-OCT-1997; 97US-0063870.  
 PR 31-OCT-1997; 97US-0064103.  
 PR 03-NOV-1997; 97US-0064248.  
 PR 07-NOV-1997; 97US-0064809.  
 PR 12-NOV-1997; 97US-0065186.  
 PR 17-NOV-1997; 97US-0065846.  
 PR 18-NOV-1997; 97US-0065693.  
 PR 21-NOV-1997; 97US-0066120.  
 PR 21-NOV-1997; 97US-0066364.  
 PR 24-NOV-1997; 97US-0066772.  
 PR 24-NOV-1997; 97US-0066466.  
 PR 24-NOV-1997; 97US-0066770.  
 PR 24-NOV-1997; 97US-0066511.  
 PR 24-NOV-1997; 97US-0066453.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;  
 XX  
 DR WFI; 1999-229533/19.  
 DR N-PSDB; AAX52221.  
 XX

CC may be conjugated to a toxin, chemotherapeutic agent or radioisotope.  
CC Genes expressing (I), many of which are growth factor homologues, are  
CC overexpressed in some cases of cancer.

CC 361 ipggvssglrmgavpvmvpaqsgslv 390  
Db

SQ Sequence 390 AA;

RESULT 3

ID AAY05286 standard; Protein; 390 AA.

ID AAY05286 standard; Protein; 390 AA.

XX Query Match 100.0%; Score 2012; DB 20; Length 390;

XX Best Local Similarity 100.0%; Pred. No. 5.8e-143;

XX Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 22-JUN-1999 (first entry)

XX EGF-like homologue PRO246.

XX EGF-like homologue PRO246.

XX KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261;

XX KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261;

XX KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;

XX KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;

XX KW FGF-8 homologue.

XX KW FGF-8 homologue.

XX OS Homo sapiens.

XX OS Homo sapiens.

XX PN W09914327-A2.

XX PN W09914327-A2.

XX PD 25-MAR-1999.

XX PD 25-MAR-1999.

XX PF 10-SEP-1998; 98WO-US18824.

XX PF 10-SEP-1998; 98WO-US18824.

XX PR 25-NOV-1997; 97US-0066840.

XX PR 25-NOV-1997; 97US-0066840.

XX PR 17-SEP-1997; 97US-0059114.

XX PR 17-SEP-1997; 97US-0059114.

XX PR 18-SEP-1997; 97US-0059263.

XX PR 18-SEP-1997; 97US-0059263.

XX PR 15-OCT-1997; 97US-0062125.

XX PR 15-OCT-1997; 97US-0062125.

XX PR 17-OCT-1997; 97US-0062285.

XX PR 17-OCT-1997; 97US-0062285.

XX PR 17-OCT-1997; 97US-0062287.

XX PR 17-OCT-1997; 97US-0062287.

XX PR 24-OCT-1997; 97US-0062816.

XX PR 24-OCT-1997; 97US-0062816.

XX PR 29-OCT-1997; 97US-0063704.

XX PR 29-OCT-1997; 97US-0063704.

XX PA (GETH ) GENENTECH INC.

XX PA (GETH ) GENENTECH INC.

XX PI Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA;

XX PI Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA;

XX PI Roy M, Wood WI;

XX PI Roy M, Wood WI;

XX WPI; 1999-229532/19.

XX WPI; 1999-229532/19.

XX N-PSDB; AAY28436.

XX N-PSDB; AAY28436.

XX Antibodies against specific proteins overexpressed in tumours

XX Antibodies against specific proteins overexpressed in tumours

XX Example 1; Fig 27; 130pp; English.

XX Example 1; Fig 27; 130pp; English.

XX This sequence represents the EGF-like homologue PRO246.

XX This sequence represents the EGF-like homologue PRO246.

XX The invention relates to antibodies (Ab) that bind to any of the

XX The invention relates to antibodies (Ab) that bind to any of the

XX polypeptides (I) designated PRO187; PRO533; PRO214; PRO240; PRO211;

XX polypeptides (I) designated PRO187; PRO533; PRO214; PRO240; PRO211;

XX PRO230; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit

XX PRO230; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit

XX expression and/or activity of (I) are used: (i) to inhibit growth of

XX expression and/or activity of (I) are used: (i) to inhibit growth of

XX tumours; and (ii) as diagnostic/prognostic reagents for detection or

XX tumours; and (ii) as diagnostic/prognostic reagents for detection or

XX quantification of (I) in cells or tissues, by standard immunoassays,

XX quantification of (I) in cells or tissues, by standard immunoassays,

XX with

XX with

OS Homo sapiens.  
 XX WO200015666-A2.  
 PN 23-MAR-2000.  
 PD 08-SEP-1999; 99WO-US20594.  
 XX 10-SEP-1998; 98US-0099803.  
 PR 10-SEP-1998; 98WO-US18824.  
 XX (GETH) GENENTECH INC.  
 PA Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI, Botstein D;  
 PI WPI; 2000-271386/23.  
 DR N-PSDB; AAA30052.  
 XX New isolated antibodies which bind to specific polypeptides used for  
 PT diagnosis and treatment of neoplastic cell growth and proliferation -  
 XX Example 8; Fig 16; 200pp; English.  
 PS This sequence represents a human PRO246 amino acid sequence. PRO246 is  
 CC probably a cell surface virus receptor. The invention relates to  
 isolated  
 CC antibodies which bind to a polypeptide. The "PRO" polypeptides are  
 CC encoded by genes which are over expressed in the genome of tumour cells.  
 CC Vectors and host cells comprising the nucleic acid encoding the  
 CC antibodies are used in the production of the antibodies. The antibodies  
 CC and nucleic acids encoding them are used for diagnosing a tumour in a  
 CC mammal. The antibodies are used for inhibiting the growth of tumour  
 cells  
 CC and identifying compounds that inhibit a biological or immunological  
 CC activity of and/or expression of a PRO187, PRO533, PRO214, PRO240,  
 CC PRO211, PRO230, PRO261, PRO246 or PRO317 polypeptide. The antibody can  
 be  
 CC used in antibody dependent enzyme mediated prodrug therapy (ADEPT) by  
 CC conjugating the antibody to a prodrug-activating enzyme which converts  
 a  
 CC prodrug to an anti-cancer drug. The antibodies can be fluorescently  
 CC labelled and monitored by light microscopy, flow cytometry or  
 fluorimetry  
 CC for diagnosis and prognosis of tumours.  
 XX  
 SQ Sequence 390 AA;  
 Query Match 100.0%; Score 2012; DB 21; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-143;  
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps  
 0;  
 QY 1 MISLPGVLTVNLRLFLGLSALAPPSPRAQLQLHPANRLQAVEGGEVVLPAWYTLHGEV 60  
 Db 1 mislpgvltnlrlflglalsalappsraqqlhpanrlqaveggevvlpawytlhgev 60  
 QY 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTTSKPGVSLVYSGMPSRNLRLGLEGLQEKD 120

Db 61 ssaqpwevpfvmwffkqkekedqvlsvyngvtttskpgvslvysmpsrnlrlgleglqekd 120  
 QY 121 SGPYSCSVNVQDKQKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQSPRSK 180  
 Db 121 sgpyscsvnnvqdkqkarghsiktletnlvppappscrlqgvphvganvtlscqspresk 180  
 QY 181 PAVQYQWDRQLPSFQTFEPAPALDVIRGSLSLTNLSSMAGVYVCKARNEVGTAQCNVTLE 240  
 Db 181 pavqygwdrlpsfqtffapaldvirgslsltnlssmagvyvckahnevgtacnvtle 240  
 QY 241 VSTGPGRAVAGAVGTIVGLGLLAGLIVLHYHRRGKALEEPANDIKEDAIAPRTLWPWKS 300  
 Db 241 vstpggaavagavgtlvlgllaglvlyhrrgkaleepandikedaiaprtlpwps 300  
 QY 301 SDTISKNGTLSSVTSARALRPHGPPRPGALTPTPSSSQALPSPRLPTDGAHPQPIISP 360  
 Db 301 sdtiskngtlssvtsaralrphgpprpgaltptpsassqalpsriptdgaahpqpisp 360  
 QY 361 IPGGVSSSGLSRMGAVPMVMPAQSQAGSLV 390  
 Db 361 ipggvsssglsrmgavpvmvmpaqsqagslv 390  
 RESULT 5  
 AAY94999  
 ID AAY94999 standard; Protein; 390 AA.  
 XX  
 AC AAY94999;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Human secreted protein vcs1\_1, SEQ ID NO:38.  
 XX  
 KW Human; secreted protein; cancer; tumour; cardiovascular disorder;  
 KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;  
 KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;  
 KW neurodegenerative disease; asthma; contraceptive.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200011015-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 24-AUG-1999; 99WO-US19351.  
 XX  
 PR 24-AUG-1998; 98US-0097638.  
 PR 24-AUG-1998; 98US-0097659.  
 PR 09-SEP-1998; 98US-0099618.  
 PR 28-SEP-1998; 98US-0102092.  
 PR 25-NOV-1998; 98US-0109978.  
 PR 23-DEC-1998; 98US-0113645.  
 PR 23-DEC-1998; 98US-0113646.  
 PR 23-AUG-1999; 99US-0379246.  
 XX  
 PA (ALPH-) ALPHAGENE INC.  
 XX

New secreted or transmembrane proteins and polynucleotides encoding them, useful for treating neurodegenerative disorders, autoimmune diseases and cancer -  
 Claim 47; Page 296-297; 357pp; English.  
 The invention relates to 40 human secreted proteins (AAY94981-Y95020), and cDNA sequences encoding them (AA23423-A23462). The secreted proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the invention may exhibit one or more activities selected from the following:  
 cytokine activity; cell proliferation; differentiation; immune modulation; haematopoiesis regulation; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic activity; anti-inflammatory activity; and tumour inhibition activity. The proteins may be administered to patients as vaccines, and the nucleotides may be used as part of a gene therapy regime. Diseases or conditions that may be treated using the proteins or nucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, especially HIV; multiple sclerosis; rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome; insulin dependent diabetes mellitus; and allergic reactions such as asthma and anaemia. They may also be used for treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin activity may additionally be useful as contraceptives. Nucleic acid sequences of the invention may be used in chromosome mapping, and as a source of diagnostic primers and probes. The present sequence represents one of the  
 40 proteins of the invention.  
 Sequence 390 AA;  
 Query Match 100.0%; Score 2012; DB 21; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-143;  
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MSLPGPLVTLNLRFLPGLSLAPPSPQAQLQHLPANRLQAVEGGVLPAYWTLHGEV 60  
 Db 1 mslpgplvtlnlrflglisalappsaqlqlhlpnarlqaveggvlpawylhgev 60  
 Qy 61 SSSQPWEVPVFMWFFKQEKEDQVLSYINGVTTSKPGVSLVYSMPNRNLSLRLEGLQEKD 120  
 Db 61 sssqpwevpvmwffkqekedqvlsyngvttskpgvslvysmpnrnlsrlleglqekd 120  
 Qy 121 SGPYSCSVNVQDKGKGRGHSIKTLENLVLPAPPSCRRLQGVPHVGVNLTSCQSPRSK 180  
 Db 121 egpyscsvnvqdkgkgrgshsiktlelnlvppappscrlqgvphvganvltscqsprak 180

Db 1 mislpgplvtlnllrrirrigisalarapparaqiqnlpnpanrigaveggevvpawytlngeev eu  
 QY 61 SSSQPEVFPVFMWFFKQKEDQVLVSYINGVTTTSPKGVSLVYSMPSPRNLSLRLGLEQEKD 120  
 Db 61 SSSQPEVFPVFMWFFKQKEDQVLVSYINGVTTTSPKGVSLVYSMPSPRNLSLRLGLEQEKD 120  
 QY 121 SGPYSCSVNVQDKQKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQSPRSK 180  
 Db 121 sgpyscsvnvqdkqkgrghsiktlnvlpvppappscrlqgvphvganvtlscqspresk 180  
 QY 181 PAVQYQWDRQLPSFQTFPAPALDVIRGSLSLTNLSLSSAGVYVCKAHNEVGTAQCNTVLE 240  
 Db 181 pavqyqwdrlpsfqtffapaldivrgslsltnlsesmagvyvckahnevgtacnvtle 240  
 QY 241 VSTGPGAAVAGAVVGTIVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300  
 Db 241 vstgpgaaavagavvgtivglglilaglvlllyhrrgkaleepandikedaiaprtlpwps 300  
 QY 301 SDTISKNGTSLSVTSARALRPHGPPRPGALTPPSSLSSQALPSPRLPTDGAHPQIPSP 360  
 Db 301 sdtiskngtislsvtsaralrphgpprpgaltptpslssqalpseprlpttdgahppipsp 360  
 QY 361 IPGGVSSGLSRMGAVPMVPAQSQAGSIV 390  
 Db 361 ipggvssglsrmgavpmvmpaqsqagalsv 390  
 RESULT 7  
 AAB88358  
 ID AAB88358 standard; Protein; 390 AA.  
 XX  
 AC AAB88358;  
 XX  
 DT 23-MAY-2001 (first entry)  
 XX  
 DE Human membrane or secretory protein clone PSEC0086.  
 XX  
 KW Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1067182-A2.  
 XX  
 PD 10-JAN-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-0114090.  
 XX  
 PR 08-JUL-1999; 99JP-0194179.  
 PR 11-JAN-2000; 2000JP-0118775.  
 PR 02-MAY-2000; 2000JP-0183766.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayaashi K;  
 XX  
 DR WPI; 2001-093989/11.  
 DR N-PSDB; AAF93785.

PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2001-408281/43.  
 DR N-PSDB; AAS21412.  
 XX  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical  
 XX  
 PS Claim 12; Fig 338; 813pp; English.  
 XX  
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, the release of a cytokine from peripheral blood  
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.  
 XX  
 SQ Sequence 390 AA;  
 Query Match 100.0%; Score 2012; DB 22; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-143;  
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps  
 0;  
 QY 1 MISLPGPLVTNLLRFLFLGLSALAPPSPRAQLQLHLHPANRLQAVEGGEVVLPAWYTLHGEV 60  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

8



QY 61 SSSQWEPVPMWFFKQKEKEDQVLSYINGVTTTSKPGVSLVSYMPRNLSRLGLEQEKD 120  
|||  
Db 61 ssgpwpvpfvmwffkqkedqvlsyngvtttskpgvslvymprnlslrlgleqekd 120  
|||  
QY 121 SGPYSCSVNVQDKQKSRGHSIKITLNLVLPVPAPPSCRLQGVPHVGVANVTLSQSPRSK 180  
|||  
Db 121 sgpyscsvnmvqdkqksrghsiktlnlvlpvpappscrlqgvphvganvtlscqspgsk 180  
|||  
QY 181 PAVQYQWDRQLPSFQTFPAFDVIRGSLSTNLSSMAGVYVCKAHNEVGTACNVTL 240  
|||  
Db 181 pavqyqwdrlpsfqtffapaldivrgslstnlssmagvyvckahnevgtacqnvtle 240  
|||  
QY 241 VSTGGAADVAGAVVGTGLVGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300  
|||  
Db 241 vstggaaadvagavvgtglvlgllaglvlllyhrrgkaleepandikedaiaprtlpwpgks 300  
|||  
QY 301 SDTISKNGTLSSVTSARALRPHGPPRPGALTPTPSLSSQALPSRLPTDGAHPQIPISP 360  
|||  
Db 301 sdtiskngtlssvtsaralrphgpprpgaltptpslssqalpsrlpttdgahpqpisp 360  
|||  
QY 361 IPGVSSSSGLSRMGAVPMVPAQSQAGSLV 390  
|||  
Db 361 ipgvsssglarmgavpmvmpaqsqagslv 390  
|||

RESULT 10

AAB80219

ID AAB80219 standard; Protein; 390 AA.

XX

AC AAB80219;

XX

DT 24-APR-2001 (first entry)

XX

DE Human PRO246 protein.

XX

KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;

KW antiparkinsonian nootropic; neuroprotective; vulnery; cardiant;

KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;

KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;

KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;

KW ischaemia; inflammation.

XX

OS Homo sapiens.

XX

PN WO200104311-A1.

XX

PD 18-JAN-2001.

XX

PF 22-FEB-2000; 2000WO-US04414.

XX

PR 07-JUL-1999; 99US-0143048.

PR

PR 26-JUL-1999; 99US-0145698.

PR

PR 28-JUL-1999; 99US-0146222.

PR

PR 08-SEP-1999; 99WO-US20594.

PR

PR 13-SEP-1999; 99WO-US20944.

PR 07-DEC-1999; 99US-0169495.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.

XX (GETH ) GENENTECH INC.

PA

XX

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;

PI Ferraza N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;

PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;

PI Wood WI, Zhang Z;

XX WPI; 2001-050091/06.

DR N-PSDB; AAC87040.

XX

PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a transmembrane polypeptide is useful for gene therapy and identification of related polypeptides -

XX

PS Claim 12; Fig 58; 24app; English.

XX

CC The present sequence represents a human secreted and transmembrane polypeptide. The specification describes human polypeptides, designated PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288, PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170, PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187, PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003, PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells can be modulated with agents that bind to these polypeptides, resulting in the death of the cells. The polynucleotides encoding these polypeptides are useful in the recombinant production of the polypeptides, as a hybridisation probe to screen libraries to isolate homologous sequences, or to map the gene. They may also be used for analysing genetic disorders, and to produce transgenic animals which are useful for the development and screening of therapeutically useful reagents. The polynucleotides can also be used in gene therapy e.g. to replace a defective gene.

XX

SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 22; Length 390;  
Best Local Similarity 100.0%; Pred. No. 5.8e-143;  
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSLEPGIVNLLRFLFLGLSALAPPSSRAQLQLHLPANRLQAVEGGEVLPANWYTLHGEV 60

PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 05-JAN-2000; 99WO-US00219.  
  
(GETH ) GENENTECH INC.  
  
PI Aabkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin LJ;  
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
PI Williams PM, Wood WI;  
  
XX WPI; 2001-081051/09..  
DR N-PSDB; AAF72379.  
  
XX Sixty one nucleic acids encoding PRO polypeptides which are useful in  
PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung  
PT squamous cell carcinoma) and neurodegenerative diseases (e.g.  
PT Alzheimer's disease) -  
  
XX Claim 1; Fig 17; 393pp; English.  
  
PS The present sequence is one of sixty one novel secreted and  
XX transmembrane PRO polypeptides. The PRO polypeptides are  
CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung  
CC squamous cell carcinoma), gastrointestinal disorders (e.g.  
CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,  
CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.  
CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,  
CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and  
CC diabetes and retinal disorders such as retinitis pigmentosa.  
CC The PRO nucleic acids have applications in molecular biology, including  
CC use as hybridization probes, and in chromosome and gene mapping.  
  
XX Sequence 390 AA;  
SQ  
  
Query Match 100.0%; Score 2012; DB 22; Length 390;  
Best Local Similarity 100.0%; Pred. No. 5.8e-143;  
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps  
0;  
  
QY 1 MISLPGPLVTLNLRFLFLGLSALAPPSPRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60  
Db 1 mislpgplvtlnlrflflglsalappsqraqqlhlpnrlqaveggevvlpawylhgev 60  
  
QY 61 SSSQPWEVFPVMWFVKQKEKEDQVLSYINGVTTTSKPGVSLVSNPRLSLRLEGLQEKD 120  
Db 61 ssqgpwevpvmwffkqkqekedqvlsyngvtttskpgvalvsnprslrlrleglqekd 120  
  
QY 121 SGFYSCSVNVQDKQKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGNVTLSCQSPRSK 180

Db 121 sgpyacevvnvdkgkqkargheiktielelnvlyppappscrlgvyphvganvtlscqgsprsk 180  
  
QY 181 PAVQYQWDRQLPSPQTFPPAPALDVIRGSLISLTNLSSSMAGVYVCKAHNEVGTACQNVTL 240  
Db 181 pavqyqwdrglpqsfqtfppaldvirgslsltnlsssmagvyvckahnevgtacqnvtle 240  
  
QY 241 VSTGPGAAVAVAGVGTGLVGLLGLAGLVLLYHRRGKALEEPANDIKEDAIAIARTLTPWPKS 300  
Db 241 vstgpgaaavagavgtglvlgllglaglvlllyhrrgkaleepandikedaiartltpwps 300  
  
QY 301 SDTISKNGTLSSVTSARALRPPHPPRPGALTPPTPSLSSQALPSPRLPTTDCGAHPDIPSP 360  
Db 301 sdtiskngtltssvtsaralrpphpprpgaltptpslssqalpsprlpttgcgahpdpisp 360  
  
QY 361 IPGGVSSSGLSRMGAVPMVMPAQSQAGSLV 390  
Db 361 ipggvasaglsrmgavpmvmpaqsqagslv 390  
  
RESULT 11  
AAB53082  
ID AAB53082 standard; Protein; 390 AA.  
XX  
AC AAB53082;  
XX  
DT 28-FEB-2001 (first entry)  
XX  
DE Human angiogenesis-associated protein PRO246, SEQ ID NO:96.  
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal.  
XX  
OS Homo sapiens.  
XX  
PN WO200053753-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000WO-US00219.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.

(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA, Paoni NP, Picti RM, Watanabe CK, Williams PM, Wood WI;

WPI; 2001-090793/10.  
N-PSDB; AAC97441.

New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer -

Claim 69; Fig 38; 293pp; English.

The invention relates to novel human angiogenesis-associated proteins designated PRO-proteins (AA853064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO protein, agonists or antagonists of a PRO protein, and compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or PRO agonist or antagonist; a retroviral gene therapy vector comprising

PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins,

to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents. The present sequence represents a PRO protein of the invention.

Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 22; Length 390;

|                |             |                                                                          |     |
|----------------|-------------|--------------------------------------------------------------------------|-----|
| QY             | 1           | MISLPGPLVTNLLRFLFLGLSALAPPSPRAQLQHLHPANLQAVEGGEVVLPAWTLHGEV              | 60  |
| Db             | 1           | misalpplvtlnllrflflglsalappsraqqlhlpnlrlqaveggevlpawtytlhgev             | 60  |
| QY             | 61          | SSSQPWEVPFVMWFFKQEKEDQVLSYINGVTTSTKPGVSLVYSFSPRNLSLRLEGLQEKD             | 120 |
| Db             | 61          | sssqpwevpfvmwffkqekedqvlslsyngvttstkgvalvyamparnlsrlrleqlqekd            | 120 |
| QY             | 121         | SGPYSCSVNVQDKQKSRGHSIKTLENLVLPAPPSCRLQGVHPHVGANVTLSQSPRSK                | 180 |
| Db             | 121         | sgpyscsvnvqdkgksrgshsiktelnlvppappscrlqgvphvganvtlscqsprsk               | 180 |
| QY             | 181         | PAVQYQWDRQLPSQTFPAPALDVIRGSLTNLSSSMAGVYVCAHNEVGTACNVTLLE                 | 240 |
| Db             | 181         | pavgyqwdrlpsqtfpaldvirgsltnlsssmagvyvckahnevgtacnvtlle                   | 240 |
| QY             | 241         | VSTGPAAVAVAGVGTTLVGLGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS              | 300 |
| Db             | 241         | vstgpaaavagavvgttlvglglaglvlllyhrrgkaleepandikedaiaprtlpwpsk             | 300 |
| QY             | 301         | SDTISKNGTSSVTSARALRPPHGPDPGALTPTPSLSSQALPSPRLPTTGAHPQIPSP                | 360 |
| Db             | 301         | sdtiskngtssvtsaralrpphgpdpgaltptpslssqalsprrlpttdgahpqpisp               | 360 |
| QY             | 361         | IPGGVSSSGLSRMGAVPMVPAQSQAGSLV                                            | 390 |
| Db             | 361         | ipggvsssglrmgavpmvpaqsqagslv                                             | 390 |
| RESULT         | 12          |                                                                          |     |
| AAE06610       |             |                                                                          |     |
| ID             | AAE06610    | standard; Protein; 390 AA.                                               |     |
| XX             |             |                                                                          |     |
| AC             | AAE06610;   |                                                                          |     |
| XX             |             |                                                                          |     |
| DT             | 25-SEP-2001 | (first entry)                                                            |     |
| XX             |             |                                                                          |     |
| DE             |             | Human protein having hydrophobic domain, HP10801.                        |     |
| XX             |             |                                                                          |     |
| KW             |             | Human; hydrophobic domain; gene therapy; nutritional supplement;         |     |
| KW             |             | cell proliferation; immunomodulatory; autoimmune disorder;               |     |
| antimicrobial; |             |                                                                          |     |
| KW             |             | multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;    |     |
| KW             |             | haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; |     |
| KW             |             | Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;    |     |
| KW             |             | haemostatic; thrombolytic; tumour growth inhibitor; anabolic;            |     |
| KW             |             | contraceptive; antiinfertility; antiinflammatory.                        |     |
| XX             |             |                                                                          |     |
| OS             |             | Homo sapiens.                                                            |     |
| XX             |             |                                                                          |     |
| PH             | Key         | Location/Qualifiers                                                      |     |
| FT             | Peptide     | 1..30                                                                    |     |
| FT             |             | /label= Signal_peptide                                                   |     |
| FT             | Protein     | 31..390                                                                  |     |

PI Kuga T, Sekine S, Nakamura Y, Sugano S;  
XX  
DR WPI; 2001-266308/27.  
DR N-PSDB; AAH02949.  
XX  
PT DNA sequences, proteins encoded by them and antibodies against them  
PT useful in diagnosis and treatment of vascular disease caused by  
PT arteriosclerosis -  
XX  
PS Claim 35; Page 599-601; 678pp; Japanese.  
XX  
CC The present invention provides the protein and coding sequences of a  
CC number of human shear stress response proteins. These are useful in the  
CC diagnosis, treatment and screening of vascular diseases caused by  
CC arteriosclerosis, including heart failure, post-PTCA restenosis and  
CC hypertension.  
XX  
SQ Sequence 390 AA;  
  
Query Match 99.6%; Score 2004; DB 22; Length 390;  
Best Local Similarity 99.7%; Pred. No. 2.3e-142;  
Matches 389; Conservative 0; Mismatches 1; Indels 0; Gaps  
0;  
QY 1 MISLPGPLVTLNLLRFLGLSALAPPSSRAQLQLHLPANRLQAVGEGVVLPWYTLHGVEV 60  
Db 1 mislpgplvtlnllrflglalappsraqqlhlpanrlqaveggevlpawtytlhgev 60  
QY 61 SSSQPEVDFVMWFFKQEKEDQVLSYINGVTTSKPGVSLVYSPSRNLRLRLEGLQEKD 120  
Db 61 sssqpewdfvmwffkqekedqvlsyngvttskpgvslvyspsrnlrlrleglqekd 120  
QY 121 SGYSCSVNVQDKQKGRHSIKITLNLVLPAPPSCRLQGVPHVGVANVTLSQSPRSK 180  
Db 121 sgpyscsvnvqdkqkgrhsiktlnlvppappscrlqgvphvganvtlscqsprsk 180  
QY 181 PAVQYQWDRQLPSQTFPPALDVIRGSLTLNLSSSMAGVYVCKAHNEVGTACQNVTL 240  
Db 181 pavqyqwdrlpsqtfppaldvirgsltlnlsssmagvyvckahnevgtacqnvtle 240  
QY 241 VSTGFGAAVVAGAVVGTGLVGLGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300  
Db 241 vstgfgaavvagavvgtglvglglaglvllyhrrgkaleepandikedaiaprtlpwps 300  
QY 301 SDTISKNGTLSSVTSARALRPPHGPGRGALTPTPSLSSQALPSRLPTTDGAHPQIPSP 360  
Db 301 sdtiskngtlssvtsaralrpphgpgrgaltptpslssqalpsrlpttdgahppisp 360  
QY 361 IPGGVSSSGLSRMGAVPMVPAQSQAGSLV 390  
Db 361 ipggvsssglsrmgavpmvmpaqsqagslv 390  
  
RESULT 14  
AAAY76303  
ID AAAY76303 standard; Protein; 389 AA.

AC AAY76303;  
XX  
DT 23-MAR-2000 (first entry)  
XX  
DE Fragment of human secreted protein encoded by gene 29.  
XX  
KW Human; secreted protein; cancer; tumour; developmental abnormality;  
KW foetal deficiency; blood disorder; immune system disorder; inflammation;  
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;  
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;  
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;  
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;  
KW therapy.  
XX  
OS Homo sapiens.  
XX  
PN W09958660-A1.  
XX  
PD 18-NOV-1999.  
XX  
PF 06-MAY-1999; 99WO-US09847.  
XX  
PR 12-MAY-1998; 98US-0085093.  
PR 12-MAY-1998; 98US-0085094.  
PR 12-MAY-1998; 98US-0085105.  
PR 12-MAY-1998; 98US-0085180.  
PR 18-MAY-1998; 98US-0085906.  
PR 18-MAY-1998; 98US-0085920.  
PR 18-MAY-1998; 98US-0085921.  
PR 18-MAY-1998; 98US-0085922.  
PR 18-MAY-1998; 98US-0085923.  
PR 18-MAY-1998; 98US-0085924.  
PR 18-MAY-1998; 98US-0085928.  
PR 18-MAY-1998; 98US-0085925.  
PR 18-MAY-1998; 98US-0085927.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;  
PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;  
PI Lafleur DW, Endress GA, Ebner R;  
XX  
WPI; 2000-062296/05.  
XX  
PT New isolated human genes and the secreted polypeptides they encode,  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders -  
XX  
PS Disclosure; Page 440-441; 475pp; English.  
XX  
CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.  
CC AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human  
CC genes. This sequence represents a fragment of one of the human secreted  
CC proteins. The genes and their corresponding secreted polypeptides are  
CC useful for preventing, treating or ameliorating secreted polypeptides are  
CC e.g. by protein or gene therapy. Also pathological conditions can be  
CC diagnosed by determining the amount of the new polypeptides in a sample

PT XX /note= "Mature human protein with hydrophobic domain"

WO200149728-A2.  
12-JUL-2001.  
28-DEC-2000; 2000WO-JP09359.  
06-JAN-2000; 2000JP-0000585.  
06-JAN-2000; 2000JP-0000588.  
11-JAN-2000; 2000JP-0002299.  
03-FEB-2000; 2000JP-0026862.  
03-MAR-2000; 2000JP-0058367.  
(PROT-) PROTEGENE INC.  
(SAGA ) SAGAMI CHEM RES CENT.  
Kato S, Kimura T;  
WPI; 2001-418355/44.  
N-PSDB; AAD12605.  
Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -  
Claim 1; Page 448-450; 563pp; English.  
The present sequence is human protein with hydrophobic domain, HP10801. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate haematopoiesis, to modulate tissue growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling fertility), to modulate chemotactic and chemokinetic activity, to modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.  
SQ Sequence 390 AA;  
Query Match 99.6%; Score 2004; DB 22; Length 390;  
Best Local Similarity 99.7%; Pred. No. 2.3e-142;

|           |                                                                              |
|-----------|------------------------------------------------------------------------------|
|           | Matches 389; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                 |
| QY        | 1 MISLPGPLVTLNLLRFLGLSALAPPSPRAQLQLHLHPANRLQAVEGGEVTLPAWYTLHGEV 60<br>       |
| Db        | 1 mislpgplvtlnllrfiflgisalappsraqqlhlpnriqaveggevlpawtylhgev 60<br>          |
| QY        | 61 SSSQPWEVPFVWFFKQKEKEDQVLSYINGVTTTSKPGVSLVYSPSRNLSRLGLEQEKD 120<br>        |
| Db        | 61 sssqpwevpfvmwffkqkekedqvlsyngvtttskpgvslvyspsrnlslrlgleqekd 120<br>       |
| QY        | 121 SGPYSCSVNVQDKQKSRGHSIKITLNLNLVPPAPPSCRLQGVPHVGANVTLSQCSPRSK 180<br>      |
| Db        | 121 sgpyscsvnvqdkqksrghsikitlelnlvppappscrlqgvphvganvtlscqsprsk 180<br>      |
| QY        | 181 PAVQYQWDRQLPSFQTFPAPALDVIRGSLSTNLSSMAGVYVCKAHNEVGTAQCNTLE 240<br>        |
| Db        | 181 pavqyqwdrlpsfqtffapaldvirgslstnlssmagvyvckahnevgtaqcnvle 240<br>         |
| QY        | 241 VSTGPGAAGVAVGVTLVGLLGLLHVRGRKALEEPANDIKEDAIAPRTLPWPKS 300<br>            |
| Db        | 241 vstgpgaavvagvgtlvglglhvrgrkaleepandikedaiaprtlpwps 300<br>               |
| QY        | 301 SDTISKNGTLSSVTSARALRPHGPPRPGALTPPSLSSQALPSPRLPTDGAHPQPTSP 360<br>        |
| Db        | 301 sdtiskngtlssvtsaralrphgpprpgaltptpslssqalpsprlpttdgahppqisp 360<br>      |
| QY        | 361 IPGGVSSSGLSRMGAVPMVMPAQSQAGSLV 390<br>                                   |
| Db        | 361 ipggvsssglsrmgavpvmvmpaqsqagalv 390<br>                                  |
| RESULT 13 |                                                                              |
| AAB90818  | ID AAB90818 standard; Protein; 390 AA.                                       |
| XX        | AC AAB90818;                                                                 |
| XX        | DT 15-JUN-2001 (first entry)                                                 |
| XX        | DE Human shear stress-response protein SEQ ID NO: 144.                       |
| XX        | KW Human; shear stress-response protein; vascular disease; arteriosclerosis. |
| XX        | OS Homo sapiens.                                                             |
| XX        | PN WO200125427-A1.                                                           |
| XX        | PD 12-APR-2001.                                                              |
| XX        | PF 02-OCT-2000; 2000WO-JP06840.                                              |
| XX        | PR 01-OCT-1999; 99JP-0280976.                                                |
| XX        | PA (KYOW ) KYOWA HAKKO KOGYO KK.                                             |
| XX        | PA (NOJI/) NOJIMA H.                                                         |

|        |                                   |
|--------|-----------------------------------|
| AB5832 | AB5832 standard; protein; 370 kDa |
| AB5832 | AB5832                            |
| ID     | AB5832                            |
| XX     | XX                                |
| AC     | AB5832;                           |

[illegible]

|    |     |             |         |        |          |        |          |        |        |     |
|----|-----|-------------|---------|--------|----------|--------|----------|--------|--------|-----|
| QY | 241 | VSTGPGAAVVA | GAVVGT  | LVGLGL | LVLYHRRG | KALEEP | PANDIKED | ALPRTL | PWPKS  | 300 |
|    |     |             |         |        |          |        |          |        |        |     |
| Db | 241 | vstgpgaa    | vvaevgt | lvglgl | lvlyhrrg | kaleep | pandiked | alprtl | pwpk   | 300 |
| QY | 301 | SDTISNGT    | SVTSAR  | LRPPH  | GPRPGAL  | TPPSIS | SQLPSPR  | -----  | LPTTGA | 353 |
|    |     |             |         |        |          |        |          |        |        |     |
| Db | 301 | sdtskngt    | svtsara | lrpph  | gpprgal  | tppls  | sqalps   | prhndi | wgppet | 360 |
| QY | 354 | HP          | 355     |        |          |        |          |        |        |     |
|    |     |             |         |        |          |        |          |        |        |     |
| Db | 361 | hp          | 362     |        |          |        |          |        |        |     |

Search completed: August 19, 2002, 17:09:06  
 Job time: 3349 sec

OM protein - protein search, using sw model

Run on: August 19, 2002, 16:16:12 ; Search time 24.02 Seconds  
(without alignments)  
396.585 Million cell  
updates/sec

Title: US-09-902-759-39  
Perfect score: 2012  
Sequence: 1 MISLPGLVTNLLRFLFGL.....SRMGAVPMVPAQSQAGSLV 390

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID                  | Description       |
|------------|-------|-------------|--------|---------------------|-------------------|
| 1          | 2012  | 100.0       | 390    | 2 US-08-979-424-1   | Sequence 1, Appli |
| 2          | 353.5 | 17.6        | 365    | 4 US-08-928-383B-26 | Sequence 26, Appl |
| 3          | 346   | 17.2        | 365    | 4 US-08-928-383B-2  | Sequence 2, Appli |
| 4          | 345.5 | 17.2        | 365    | 4 US-08-928-383B-23 | Sequence 23, Appl |
| 5          | 343   | 17.0        | 365    | 2 US-08-979-424-3   | Sequence 3, Appli |
| 6          | 343   | 17.0        | 365    | 4 US-09-272-496-2   | Sequence 2, Appli |
| 7          | 297   | 14.8        | 319    | 1 US-08-597-495B-22 | Sequence 22, Appl |
| 8          | 297   | 14.8        | 319    | 4 US-09-068-051A-22 | Sequence 22, Appl |
| 9          | 290.5 | 14.4        | 365    | 4 US-08-928-383B-24 | Sequence 24, Appl |
| 10         | 289.5 | 14.4        | 387    | 4 US-09-175-928-2   | Sequence 2, Appli |
| 11         | 258   | 12.8        | 318    | 4 US-09-068-051A-32 | Sequence 32, Appl |

12 176 8.7 299 4 US-09-188-930-331  
13 176 8.7 299 4 US-09-462-270-2  
14 171 8.5 299 4 US-09-188-930-189  
15 158.5 7.9 501 2 US-08-408-095-31  
16 153.5 7.6 344 2 US-08-602-725-34  
17 152 7.6 1101 3 US-08-986-485-2  
18 134 6.7 607 2 US-08-752-307B-12  
19 133 6.6 321 6 5169835-17  
20 133 6.6 464 2 US-08-602-725-32  
21 133 6.6 642 1 US-08-217-299-1  
22 133 6.6 698 2 US-08-602-725-36  
23 133 6.6 734 2 US-08-389-459A-17  
24 133 6.6 734 3 US-08-987-867A-17  
25 132.5 6.6 252 2 US-08-414-657D-56  
26 132.5 6.6 287 2 US-08-414-657D-48  
27 132.5 6.6 304 2 US-08-414-657D-44  
28 132.5 6.6 308 2 US-08-414-657D-46  
29 132.5 6.6 325 2 US-08-414-657D-2  
30 132.5 6.6 325 2 US-08-414-657D-41  
31 132.5 6.6 338 2 US-08-414-657D-60  
32 132.5 6.6 1241 4 US-09-040-774-2  
33 132 6.6 828 1 US-08-261-304-2  
34 130 6.5 1091 3 US-08-986-485-5  
35 129 6.4 917 1 US-08-245-295-2  
36 129 6.4 917 1 US-08-481-130-2  
37 129 6.4 917 1 US-08-656-984A-2  
38 129 6.4 917 1 US-08-485-604-2  
39 129 6.4 917 2 US-08-487-595-2  
40 128.5 6.4 252 2 US-08-414-657D-57  
41 128.5 6.4 287 2 US-08-414-657D-49  
42 128.5 6.4 310 2 US-08-414-657D-45  
43 128.5 6.4 315 2 US-08-414-657D-47  
44 128.5 6.4 338 2 US-08-414-657D-42  
45 128.5 6.4 338 2 US-08-414-657D-43

ALIGNMENTS

RESULT 1  
US-08-979-424-1  
; Sequence 1, Application US/08979424  
; Patent No. 5942606  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/979,424  
 FILING DATE: Filed Herewith  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PP-0405, US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 390 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: LUNGFET03  
 CLONE: 1232054  
 US-08-979-424-1

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Query Match      100.0%; Score 2012; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 3.7e-168;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

QY      1  MISLPGPLVTNLLRFLGLSALAPPSSRAQLQLHLHPANRLQAVEGGEVVLPAWYTLHGEV 60
      |||||
Db      1  MISLPGPLVTNLLRFLGLSALAPPSSRAQLQLHLHPANRLQAVEGGEVVLPAWYTLHGEV 60

QY      61  SSSQPWEVPVMPFPKQEKEDQVLSYINGVTTSKPGVSLVYSPSRNLSLRLEGLQEKD 120
      |||||
Db      61  SSSQPWEVPVMPFPKQEKEDQVLSYINGVTTSKPGVSLVYSPSRNLSLRLEGLQEKD 120

QY      121  SGPYSCSVNVQDKQKSRGHSIKITLELNVLPVPPAPPSCLRQGVPHVGANVTLSQCSPRSK 180
      |||||
Db      121  SGPYSCSVNVQDKQKSRGHSIKITLELNVLPVPPAPPSCLRQGVPHVGANVTLSQCSPRSK 180

QY      181  PAVQYQWDRQLPSFOTFFAPALDVIRGSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
      |||||
Db      181  PAVQYQWDRQLPSFOTFFAPALDVIRGSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240

QY      241  VSTGPAAVVAGAVVGTLVGLGLLAGLVLLYHRRKALEEPANDIKEDAIAPRTLEFPWPKS 300
      |||||
Db      241  VSTGPAAVVAGAVVGTLVGLGLLAGLVLLYHRRKALEEPANDIKEDAIAPRTLEFPWPKS 300

QY      301  SDTISKNGTLLSVTSARALRPPHGP RP PGALTPTPSLSSQALPSRPLTTDGAHPQIPSP 360
      |||||
Db      301  SDTISKNGTLLSVTSARALRPPHGP RP PGALTPTPSLSSQALPSRPLTTDGAHPQIPSP 360

```

```

Query Match      17.6%; Score 353.5; DB 4; Length 365;
Best Local Similarity 27.8%; Pred. No. 4.7e-23;
Matches 113; Conservative 71; Mismatches 156; Indels 67; Gaps
15;

QY      9 VTNLLRFLFL-GISALAPPSPAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSSQPW 67
      : ||| : | : : : | : | : | : | : | : | : | : | : | : | :
DB      1 MARLLCFVLLCGIADFT-----SGLSITTPQRIEKAKGETAYLFCKFTLSPE--DQGP 54

```

QY 68 VPFWMPFKQKEK--DQVLSYINGVTTSKPGVSLVY-----SMPSRNL 109  
: | : : ||| : | : | :  
Db 55 IE---WLISPSDNQVDQVILYSG-----DKIYDNTYFDLKGVRHFTSNDVKS GDA 103  
: : | | | | : : | : | :  
QY 110 SLRLEGLQEKDGGPYSCSVNVQDKGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGAN 169  
: : | | | | : : | | | | : : | : | :  
Db 104 SINVTNLQSLDIGTYQCKVK-----KAPGVANKKFLLTVLVKPSGTRCFVDGSEI GND 157  
: : | | | | : : | | | | : : | : | :  
QY 170 VTLSQSPRSKPAVQYQWDRQLPSQTFAPAL-DVIRGSLSLTNLSSSMAGVYVCKAHN 228  
: : | : | : | : | : | : | : | : | : | : | :  
Db 158 FKLKCEPKESLPLQFEM-QKLSDSQTMPTPWLAEMTSPVISVKNASSEYSGTYSCTVQN 216  
: : | : | : | : | : | : | : | : | : | : | :  
QY 229 EVGTAQCNVTLE-VSTGPGAAVAGAVVGTIVGLGILAGLVLLYHRR---GKALEEPAND 284  
: : | : | : | : | : | : | : | : | : | : | :  
Db 217 RVGSDQCMRLDVPVPSNRAGTIAGAVIGTILALVLIGAILFCCHKRREEKYEKEVHHD 276  
: : | : | : | : | : | : | : | : | : | : | :  
QY 285 IKEDAIAPRTLPPWKSSDTISKNGTSSVTSARALRPPHGP RP PGALTPTPSLSQALPS 344  
: : | : | : | : | : | : | : | : | : | : | :  
Db 277 IRED-----VPPPKSRTSTARSYIGSNHSSL-----GSMSPSNMEGYSKTQY 318  
: : | : | : | : | : | : | : | : | : | : | :  
QY 345 PRLPTTDGAH-PQIPISPIPGGVSSGLSRMGAVPVMPVPAQSQAGSLV 390  
: : | : | : | : | : | : | : | : | : | : | :  
Db 319 NOVPSDFERAPQSPTLAPAKVAAPNL SRMGAVPVMPVPAQSKDGSIV 365  
: : | : | : | : | : | : | : | : | : | : | :

Search completed: August 19, 2002, 17:09:51  
Job time: 3219 sec

OM protein - protein search, using sw model

Run on: August 19, 2002, 16:21:32 ; Search time 42.75 Seconds  
(without alignments)  
876.604 Million cell

updates/sec

Title: US-09-902-759-39

Perfect score: 2012

Sequence: 1 MISLPGPLVTLRLRLFLGL.....SRMGAVPMVPAQSQAGSLV 390

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 176   | 8.7         | 299    | 2 S56749 | junctional adhesio |
| 2          | 162.5 | 8.1         | 344    | 2 A27691 | nonspecific cross- |
| 3          | 158.5 | 7.9         | 847    | 2 JH0371 | B-cell adhesion pr |
| 4          | 155.5 | 7.7         | 3707   | 2 S18252 | heparan sulfate pr |
| 5          | 154.5 | 7.7         | 4391   | 2 A38096 | perlecan precursor |
| 6          | 153.5 | 7.6         | 647    | 2 A35648 | B-cell adhesion pr |
| 7          | 153.5 | 7.6         | 1040   | 2 A49356 | transient axonal   |
| 8          | 152.5 | 7.6         | 521    | 2 S34338 | biliary glycoprote |
| 9          | 152   | 7.6         | 483    | 2 T17346 | hypothetical prote |
| 10         | 151.5 | 7.5         | 1036   | 2 S22383 | axinin 1 precursor |
| 11         | 151.5 | 7.5         | 4162   | 2 T42633 | connectin/titin -  |
| 12         | 150.5 | 7.5         | 521    | 2 JCI508 | biliary glycoprote |

|    |       |     |       |          |                    |
|----|-------|-----|-------|----------|--------------------|
| 14 | 150   | 7.5 | 868   | 2 A46512 | U244 homolog/b sym |
| 15 | 149.5 | 7.4 | 341   | 2 JCI512 | biliary glycoprote |
| 16 | 147   | 7.3 | 5175  | 2 T20992 | hypothetical prote |
| 17 | 147   | 7.3 | 5198  | 2 T43290 | hemocentin precurs |
| 18 | 144   | 7.2 | 349   | 2 A34815 | carcinoembryonic   |
| a  |       |     |       |          |                    |
| 19 | 143   | 7.1 | 862   | 2 I49583 | differentiation an |
| 20 | 142   | 7.1 | 278   | 2 A39037 | carcinoembryonic   |
| a  |       |     |       |          |                    |
| 21 | 141.5 | 7.0 | 26926 | 1 I38344 | titin, cardiac mus |
| 22 | 141   | 7.0 | 458   | 2 JCI509 | biliary glycoprote |
| 23 | 139   | 6.9 | 458   | 1 WMSR1  | biliary glycoprote |
| 24 | 138.5 | 6.9 | 495   | 2 A55181 | pregnancy-specific |
| 25 | 138.5 | 6.9 | 1323  | 2 PN0568 | connectin 3B - chi |
| 26 | 138   | 6.9 | 278   | 2 JCI506 | biliary glycoprote |
| 27 | 138   | 6.9 | 419   | 2 B54312 | pregnancy-specific |
| 28 | 137   | 6.8 | 7962  | 2 I38346 | elastic titin - hu |
| 29 | 136.5 | 6.8 | 518   | 2 JC4024 | poliovirus recepto |
| 30 | 135.5 | 6.7 | 426   | 2 C55181 | pregnancy-specific |
| 31 | 135.5 | 6.7 | 426   | 2 B35334 | pregnancy-specific |
| 32 | 135   | 6.7 | 428   | 2 JS0032 | pregnancy-specific |
| 33 | 135   | 6.7 | 428   | 2 I57486 | pregnancy-specific |
| 34 | 134   | 6.7 | 240   | 2 JC4121 | pregnancy-specific |
| 35 | 134   | 6.7 | 436   | 2 B55181 | pregnancy-specific |
| 36 | 133   | 6.6 | 321   | 2 JH0395 | biliary glycoprote |
| 37 | 133   | 6.6 | 351   | 2 JH0396 | biliary glycoprote |
| 38 | 133   | 6.6 | 417   | 2 JH0394 | biliary glycoprote |
| 39 | 133   | 6.6 | 419   | 2 A36109 | pregnancy-specific |
| 40 | 133   | 6.6 | 464   | 2 C30127 | transmembrane carc |
| 41 | 133   | 6.6 | 526   | 1 A32164 | biliary glycoprote |
| 42 | 133   | 6.6 | 702   | 2 A36319 | carcinoembryonic   |
| a  |       |     |       |          |                    |
| 43 | 132.5 | 6.6 | 166   | 2 A33402 | pregnancy-specific |
| 44 | 132.5 | 6.6 | 338   | 2 JC4776 | limbic-system-asso |
| 45 | 132.5 | 6.6 | 338   | 2 JCI238 | oploid-binding pro |

#### ALIGNMENTS

RESULT 1

S56749

junctional adhesion molecule precursor - human

N;Alternate names: FII platelet antigen; platelet adhesion molecule PAM-1;

Platelet FII receptor

C;Species: Homo sapiens (man)

C;Date: 27-Oct-1995 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002

C;Accession: A59406; S56749

R;Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.;

Iwamatsu, A.; Kita, T.

J. Immunol. 163, 553-557, 1999

A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes

redistribution of junctional adhesion molecule in human endothelial cells.

A;Reference number: A59406; MUID:99323940; PMID:10395639

A;Accession: A59406

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-299 <OZA>  
A;Cross-references: GB:AD42050; NID:G5326797; PIDN:AD42050.1  
R;Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.  
Biochem. J. 310, 155-162, 1995  
A;Title: Mechanisms of platelet activation by a stimulatory antibody:  
cross-linking of a novel platelet receptor for monoclonal antibody F11 with  
the Fc-gamma-RII receptor.  
A;Reference number: S56749; MUID:95374438; PMID:7646439  
A;Accession: S56749  
A;Molecule type: protein  
A ; R e s i d u e s :  
28-49, 'X', 51-53; 62-73, 'E', 75-103; 123, 'F', 125-130; 'FDKDXTYLNXY', 'LT', 206, 'X'  
, 208, 'Q' <NAI>  
A;Note: the order of the peptides other than the amino terminus was not  
determined  
C;Genetics:  
A;Gene: JAM  
C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet  
membrane  
F;1-25/Domain: signal sequence #status predicted <SIG>  
F;26-299/Product: junctional adhesion molecule #status predicted <MAT>

|                       |       |                                                              |                 |                     |
|-----------------------|-------|--------------------------------------------------------------|-----------------|---------------------|
| Query Match           | 8.7%  | Score 176;                                                   | DB 2;           | Length 299;         |
| Best Local Similarity | 25.7% | Pred. No. 0.00014;                                           |                 |                     |
| Matches               | 71;   | Conservative 46;                                             | Mismatches 129; | Indels 30; Gaps 12; |
| Qy                    | 9     | VTNLRLFLGLSALAPPSRAQLQLHLPANRLQAVGGEVVLPAWYTLHGEVSSSQPWEV    | 68              |                     |
| Db                    | 7     | VERKLLCLFILAILLCSLAIGSVTVHSSEPEVRIPENNPVKLSAYS-----GFSS      | 57              |                     |
| Qy                    | 69    | PFVMWFQKQEKEDQVLSYINGVTTSKPGSVLVYSPSRNLSLRLEGLQEKDGPYSCSV    | 128             |                     |
| Db                    | 58    | PRVEWFDQGD--TTRLVCYNNKITASYE--DRVTFLEPT---GITPKSVTREDTGTTCMV | 111             |                     |
| Qy                    | 129   | NVQDKQKSRGHSIKTLELNLVPPAPPSCRLQGVPHVGANVTLSQSPSRKPAVQYQWD    | 188             |                     |
| Db                    | 112   | S--EEGNSYG-EVK-VKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTW   | 167             |                     |
| Qy                    | 189   | RQ---LP---SFQTF--FAPALDVIRGSLSTNLSSMAGVYVCKAHNEVGTQAQ-CNV    | 238             |                     |
| Db                    | 168   | KDGIWMTNPKSTRAFNSSSVYLNPTTGELVDFDPLSASDTGEYSCEARNGYGTPTMTS   | 227             |                     |
| Qy                    | 239   | LEVSTGGAADVAGAVGTIVGLGILLA-GIVLLYHR                          | 273             |                     |
| Db                    | 228   | RMEAVERNVGIVRAVLVTLILLGILVFGINPAYSR                          | 263             |                     |

Search completed: August 19, 2002, 17:10:57  
Job time: 2965 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: August 19, 2002, 17:11:02 ; Search time 24.06 Seconds  
(without alignments)  
627.624 Million cell  
updates/sec  
Title: US-09-902-759-39  
Perfect score: 2012  
Sequence: 1 MISLPGPLVTNLLRFLFLGL.....SRMGAVPMVPAQSQAGSLV 390  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES  |       |             |              |                                |
|------------|-------|-------------|--------------|--------------------------------|
| Result No. | Score | Query Match | Length DB ID | Description                    |
| 1          | 353.5 | 17.6        | 365 1        | CXAR_MOUSE P97792 mus musculus |
| 2          | 343   | 17.0        | 365 1        | CXAR_HUMAN P78310 homo sapien  |
| 3          | 297   | 14.8        | 319 1        | A33_HUMAN Q99795 homo sapien   |
| 4          | 212   | 10.5        | 298 1        | JAM2_HUMAN P57087 homo sapien  |
| 5          | 176   | 8.7         | 299 1        | JAM1_HUMAN Q9y624 homo sapien  |
| 6          | 168.5 | 8.4         | 300 1        | JAM1_MOUSE O88792 mus musculus |
| 7          | 167.5 | 8.3         | 298 1        | JAM1_BOVIN Q9xt56 bos taurus   |
| 8          | 163   | 8.1         | 344 1        | CEA6_HUMAN P40199 homo sapien  |
| 9          | 158.5 | 7.9         | 4393 1       | PGEM_HUMAN P98160 homo sapien  |
| 10         | 155.5 | 7.7         | 3707 1       | PGEM_MOUSE Q05793 mus musculus |
| 11         | 153.5 | 7.6         | 847 1        | CD22_HUMAN P20273 homo sapien  |
| 12         | 153.5 | 7.6         | 1040 1       | AXO1_HUMAN Q02246 homo sapien  |
| 13         | 151.5 | 7.5         | 1036 1       | AXO1_CHICK P28685 gallus gall  |
| 14         | 150.5 | 7.5         | 521 1        | CEA1_MOUSE P31809 mus musculus |
| 15         | 150.5 | 7.5         | 1040 1       | AXO1_RAT P22063 rattus norv    |
| 16         | 146   | 7.3         | 515 1        | PVR1_PIG Q9gl76 sus scrofa     |
| 17         | 145   | 7.2         | 517 1        | PVR1_HUMAN Q15223 homo sapien  |

|    |       |     |        |            |                     |
|----|-------|-----|--------|------------|---------------------|
| 19 | 143   | 7.1 | 862 1  | CJ22_MOUSE | P33227 mus musculus |
| 20 | 142.5 | 7.1 | 1709 1 | SN_HUMAN   | Q9b222 homo sapien  |
| 21 | 138.5 | 6.9 | 515 1  | PVR1_MOUSE | Q9jxf6 mus musculus |
| 22 | 138   | 6.9 | 348 1  | KILO_RAT   | Q920j8 rattus norv  |
| 23 | 138   | 6.9 | 419 1  | PSG4_HUMAN | Q00888 homo sapien  |
| 24 | 135.5 | 6.7 | 426 1  | PSGB_HUMAN | Q00887 homo sapien  |
| 25 | 135   | 6.7 | 428 1  | PSG3_HUMAN | Q16557 homo sapien  |
| 26 | 134.5 | 6.7 | 337 1  | G55A_CHICK | Q98892 gallus gall  |
| 27 | 133   | 6.6 | 526 1  | CEA1_HUMAN | P13688 homo sapien  |
| 28 | 133   | 6.6 | 702 1  | CEA5_HUMAN | P06731 homo sapien  |
| 29 | 132.5 | 6.6 | 338 1  | LAMP_HUMAN | Q13449 homo sapien  |
| 30 | 132.5 | 6.6 | 345 1  | OPCM_HUMAN | Q14982 homo sapien  |
| 31 | 132.5 | 6.6 | 345 1  | OPCM_RAT   | P32736 rattus norv  |
| 32 | 132   | 6.6 | 252 1  | CEA3_HUMAN | P40198 homo sapien  |
| 33 | 131.5 | 6.5 | 349 1  | LACH_SHAM  | Q26474 schistocerc  |
| 34 | 131.5 | 6.5 | 538 1  | PVR2_HUMAN | Q92692 homo sapien  |
| 35 | 131   | 6.5 | 519 1  | ECTO_RAT   | P16573 rattus norv  |
| 36 | 130.5 | 6.5 | 837 1  | NCM2_MOUSE | O35136 mus musculus |
| 37 | 130   | 6.5 | 761 1  | NCA2_HUMAN | P13592 homo sapien  |
| 38 | 130   | 6.5 | 917 1  | ICA5_MOUSE | Q60625 mus musculus |
| 39 | 129.5 | 6.4 | 345 1  | OPCM_BOVIN | P11834 bos taurus   |
| 40 | 128.5 | 6.4 | 338 1  | LAMP_RAT   | Q62813 rattus norv  |
| 41 | 128.5 | 6.4 | 837 1  | NCM2_HUMAN | O15394 homo sapien  |
| 42 | 128   | 6.4 | 338 1  | LAMP_CHICK | Q98919 gallus gall  |
| 43 | 128   | 6.4 | 530 1  | PVR2_MOUSE | P32507 mus musculus |
| 44 | 126.5 | 6.3 | 404 1  | RAGE_HUMAN | Q15109 homo sapien  |
| 45 | 126   | 6.3 | 335 1  | PSG5_HUMAN | Q15238 homo sapien  |

ALIGNMENTS

RESULT 1  
CXAR\_MOUSE  
ID CXAR\_MOUSE STANDARD; PRT; 365 AA.  
AC P97792; O09052;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Cocksackievirus and adenovirus receptor homolog precursor (mCAR).  
GN CXADR OR CAR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=97190109; PubMed=9036860;  
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,  
Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;  
RT "Isolation of a common receptor for Cocksackie B viruses and  
adenoviruses 2 and 5.";  
RL Science 275:1320-1323(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C3H/MAI;



OM protein - protein search, using sw model

Run on: August 19, 2002, 17:09:12 ; Search time 67.26 Seconds  
(without alignments)  
updates/sec 1003.093 Million cell

Title: US-09-902-759-39  
Perfect score: 2012  
Sequence: 1 MISLPGLVNLLRPLFLGL.....SRMGAVPMVPAQSQAGSLV 390

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mbc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertibrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archheap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|--------|----|----|-------------|
| -----      |       |       |        |    |    |             |

|    |       |      |     |    |        |                     |
|----|-------|------|-----|----|--------|---------------------|
| 2  | 2009  | 99.9 | 390 | 4  | Q96TSU | Q96TSU homo sapien  |
| 3  | 1931  | 96.0 | 390 | 6  | Q95KI3 | Q95KI3 macaca fasc  |
| 4  | 1397  | 69.4 | 394 | 11 | Q925F2 | Q925F2 mus musculus |
| 5  | 641.5 | 31.9 | 204 | 11 | Q9D7I2 | Q9D7I2 mus musculus |
| 6  | 343   | 17.0 | 366 | 11 | Q9DBJ8 | Q9DBJ8 mus musculus |
| 7  | 341.5 | 17.0 | 372 | 13 | Q90Y50 | Q90Y50 brachydanio  |
| 8  | 330   | 16.4 | 358 | 11 | Q9R066 | Q9R066 rattus norv  |
| 9  | 324.5 | 16.1 | 327 | 4  | Q96IQ7 | Q96IQ7 homo sapien  |
| 10 | 320.5 | 15.9 | 325 | 4  | Q95791 | Q95791 homo sapien  |
| 11 | 316   | 15.7 | 407 | 11 | Q9D2J4 | Q9D2J4 mus musculus |
| 12 | 307.5 | 15.3 | 373 | 4  | Q9H6B4 | Q9H6B4 homo sapien  |
| 13 | 290   | 14.4 | 284 | 4  | Q9NX42 | Q9NX42 homo sapien  |
| 14 | 287   | 14.3 | 373 | 11 | Q920S5 | Q920S5 mus musculus |
| 15 | 279.5 | 13.9 | 318 | 13 | Q91664 | Q91664 xenopus lae  |
| 16 | 277.5 | 13.8 | 300 | 11 | Q9D9J0 | Q9D9J0 mus musculus |
| 17 | 276.5 | 13.7 | 300 | 11 | Q9DA22 | Q9DA22 mus musculus |
| 18 | 272   | 13.5 | 352 | 11 | Q91W66 | Q91W66 mus musculus |
| 19 | 269   | 13.4 | 304 | 11 | Q9CVA4 | Q9CVA4 mus musculus |
| 20 | 267.5 | 13.3 | 328 | 11 | Q9Z109 | Q9Z109 mus musculus |
| 21 | 267.5 | 13.3 | 344 | 11 | Q9R067 | Q9R067 rattus norv  |
| 22 | 266   | 13.2 | 335 | 13 | Q9PWR4 | Q9PWR4 gallus gall  |
| 23 | 264.5 | 13.1 | 344 | 4  | Q9UKV4 | Q9UKV4 homo sapien  |
| 24 | 263   | 13.1 | 335 | 13 | Q9YGH1 | Q9YGH1 gallus gall  |
| 25 | 262.5 | 13.0 | 259 | 4  | Q95532 | Q95532 homo sapien  |
| 26 | 259   | 12.9 | 319 | 11 | Q922D5 | Q922D5 mus musculus |
| 27 | 258   | 12.8 | 319 | 6  | Q9TU80 | Q9TU80 canis famil  |
| 28 | 258   | 12.8 | 319 | 11 | Q9JKA5 | Q9JKA5 mus musculus |
| 29 | 257   | 12.8 | 248 | 11 | Q9D0T4 | Q9D0T4 mus musculus |
| 30 | 256   | 12.7 | 319 | 6  | Q9TU79 | Q9TU79 sus scrofa   |
| 31 | 253   | 12.6 | 335 | 13 | Q9YGV5 | Q9YGV5 gallus gall  |
| 32 | 221   | 11.0 | 181 | 13 | Q91665 | Q91665 xenopus lae  |
| 33 | 196   | 9.7  | 577 | 11 | Q9D2Z1 | Q9D2Z1 mus musculus |
| 34 | 186.5 | 9.3  | 977 | 4  | Q96RD9 | Q96RD9 homo sapien  |
| 35 | 183   | 9.1  | 300 | 11 | Q9JHY1 | Q9JHY1 rattus norv  |
| 36 | 176   | 8.7  | 298 | 11 | Q9J159 | Q9J159 mus musculus |
| 37 | 171   | 8.5  | 381 | 4  | Q9Y4A4 | Q9Y4A4 homo sapien  |
| 38 | 169.5 | 8.4  | 309 | 4  | Q96FL1 | Q96FL1 homo sapien  |
| 39 | 169.5 | 8.4  | 310 | 4  | Q9BX67 | Q9BX67 homo sapien  |
| 40 | 168.5 | 8.4  | 430 | 4  | Q15600 | Q15600 homo sapien  |
| 41 | 166.5 | 8.3  | 310 | 11 | Q9D8B7 | Q9D8B7 mus musculus |
| 42 | 166   | 8.3  | 310 | 11 | Q9EPK4 | Q9EPK4 mus musculus |
| 43 | 166   | 8.3  | 310 | 11 | Q9D1M9 | Q9D1M9 mus musculus |
| 44 | 164   | 8.2  | 538 | 4  | Q9NWQ7 | Q9NWQ7 homo sapien  |
| 45 | 163.5 | 8.1  | 512 | 4  | Q96DN8 | Q96DN8 homo sapien  |

ALIGNMENTS

| RESULT | 1                                                   |
|--------|-----------------------------------------------------|
| Q96AP7 |                                                     |
| ID     | Q96AP7                                              |
| AC     | Q96AP7;                                             |
| DT     | 01-DEC-2001 (TRENBLrel. 19, Created)                |
| DT     | 01-DEC-2001 (TRENBLrel. 19, Last sequence update)   |
| DT     | 01-DEC-2001 (TRENBLrel. 19, Last annotation update) |
| DE     | HYPOTHETICAL 41.2 KDA PROTEIN.                      |

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21238298; PubMed=11279107;  
 RA Hirata K.-I., Ishida T., Penta K., Rezaee M., Yang E., Wohlgenuth J.,  
 RA Quaternous T.;  
 RT "Cloning of an immunoglobulin family adhesion molecule selectively  
 expressed by endothelial cells.";  
 RL J. Biol. Chem. 276:16223-16231 (2001).  
 DR EMBL; AF361746; AAK51065.1; -.  
 SQ SEQUENCE 390 AA; 41208 MW; CSE3EB5F41B6EEC CRC64;

Query Match 99.9%; Score 2009; DB 4; Length 390;  
 Best Local Similarity 99.7%; Pred. No. 1.7e-155;  
 Matches 389; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MISLPGLVTNLLRFLFLGLSALAPPSRAQLQLHLHPANLQAVGEGVVLPAWYTLHGEV 60  
 DB 1 MISLPGLVTNLLRFLFLGLSALAPPSRAQLQLHLHPANLQAVGEGVVLPAWYTLHGEV 60  
 QY 61 SSSQPWEVFFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSPSRNLSLRLEGLQEKD 120  
 DB 61 SSSQPWEVFFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSPSRNLSLRLEGLQEKD 120  
 QY 121 SGPYSCSVNVQDKGKSRGHSIKTLELNVLVPPAPPSCRLLQGVPHVGANVTLSQSPRSK 180  
 DB 121 SGPYSCSVNVQDKGKSRGHSIKTLELNVLVPPAPPSCRLLQGVPHVGANVTLSQSPRSK 180  
 QY 181 PAVQYQWDRQLPSQTFFPAPALDVIRGSLTLNLSSSMAGVYVCKAHNEVGTACQNVTL 240  
 DB 181 PAVQYQWDRQLPSQTFFPAPALDVIRGSLTLNLSSSMAGVYVCKAHNEVGTACQNVTL 240  
 QY 241 VSTGPAAVAVAGAVVGTGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300  
 DB 241 VSTGPAAVAVAGAVVGTGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300  
 QY 301 SDTISKNGTILSSVTSARALRPPHGPAPGALTPTPSLSSQALPSRLPTTDGAHPQIPSP 360  
 DB 301 SDTISKNGTILSSVTSARALRPPHGPAPGALTPTPSLSSQALPSRLPTTDGAHPQIPSP 360  
 QY 361 IPGGVSSSGLSRMGAVPMVMPAQSQAGSLV 390  
 DB 361 IPGGVSSSGLSRMGAVPMVMPAQSQAGSLV 390

RESULT 3  
 Q95KI3  
 ID Q95KI3 PRELIMINARY; PRT; 390 AA.  
 AC Q95KI3;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL 40.9 KDA PROTEIN.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

GS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=COLON ADENOCARCINOMA;  
 RA Strausberg R.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC016868; AAH16868.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 390 AA; 41176 MW; CSE3F302F41B6EEC CRC64;

Query Match 100.0%; Score 2012; DB 4; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-156;  
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MISLPGLVTNLLRFLFLGLSALAPPSRAQLQLHLHPANLQAVGEGVVLPAWYTLHGEV 60  
 DB 1 MISLPGLVTNLLRFLFLGLSALAPPSRAQLQLHLHPANLQAVGEGVVLPAWYTLHGEV 60  
 QY 61 SSSQPWEVFFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSPSRNLSLRLEGLQEKD 120  
 DB 61 SSSQPWEVFFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSPSRNLSLRLEGLQEKD 120  
 QY 121 SGPYSCSVNVQDKGKSRGHSIKTLELNVLVPPAPPSCRLLQGVPHVGANVTLSQSPRSK 180  
 DB 121 SGPYSCSVNVQDKGKSRGHSIKTLELNVLVPPAPPSCRLLQGVPHVGANVTLSQSPRSK 180  
 QY 181 PAVQYQWDRQLPSQTFFPAPALDVIRGSLTLNLSSSMAGVYVCKAHNEVGTACQNVTL 240  
 DB 181 PAVQYQWDRQLPSQTFFPAPALDVIRGSLTLNLSSSMAGVYVCKAHNEVGTACQNVTL 240  
 QY 241 VSTGPAAVAVAGAVVGTGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300  
 DB 241 VSTGPAAVAVAGAVVGTGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300  
 QY 301 SDTISKNGTILSSVTSARALRPPHGPAPGALTPTPSLSSQALPSRLPTTDGAHPQIPSP 360  
 DB 301 SDTISKNGTILSSVTSARALRPPHGPAPGALTPTPSLSSQALPSRLPTTDGAHPQIPSP 360  
 QY 361 IPGGVSSSGLSRMGAVPMVMPAQSQAGSLV 390  
 DB 361 IPGGVSSSGLSRMGAVPMVMPAQSQAGSLV 390

RESULT 2  
 Q96T50  
 ID Q96T50 PRELIMINARY; PRT; 390 AA.  
 AC Q96T50;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ENDOTHELIAL CELL-SELECTIVE ADHESION MOLECULE.  
 GN ESAM.  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=TEMPORAL LOBE RIGHT;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
RA Suzuki Y., Sugano S., Hashimoto K.;  
RT "Isolation of full-length cDNA clones from macaque brain cDNA  
RT libraries";  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
RW EMBL; AB060855; BAB46874.1; --  
KW Hypothetical protein.  
SQ SEQUENCE 390 AA; 40946 MW; CDBF63F2BD464EF5 CRC64;

Query Match 96.0%; Score 1931; DB 6; Length 390;  
Best Local Similarity 96.4%; Pred. No. 378e-149;  
Matches 376; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MISLPGLVTLNLLRFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVLPWYTLHGEV 60  
Db 1 MISLPGLVTLNLLRFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVLPWYTLHAEV 60  
Qy 61 SSSQPWEVFFVMWFFKQEKEDQVLSYINGVTTSKPGVSLVYMPGRNLSRLGLEQEKD 120  
Db 61 SSAQPGVFFVMWFFKQEKEDQVLSYINGVTTSKPGVSLVYMPGRNLSRLGLEQEKD 120  
Qy 121 SGPYSCSVNVQDKGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGVANVTLSCQSPRSK 180  
Db 121 SGPYSCSVNVQDKGQASGHSIKTLELNVLVPPAPPSCRLQGVPHVGVANVTLSCQSPRSK 180  
Qy 181 PAVQYQWDRQLPSFQTFPAPALDVIRGSLTLNLSMAGVYVCKAHNEVGTACNVTL 240  
Db 181 PAVQYQWDRQLPSFQTFPAPALDVIRGSLTLNLSMAGVYVCKAHNEVGTACNVTL 240  
Qy 241 VSTGPGAAVAGAVVGTGLGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWP 300  
Db 241 VSTGPGAAVAGAVVGTGLGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWP 300  
Qy 301 SDTISKNGTLSSVTSARALRPPHPPGALTPPSSQALPSPRLPTTGDGAPQISP 360  
Db 301 SDTISKNGTLSSVTSARALRPPHPPGALTPPSSQALPSPRLPTTGDGAPQISP 360  
Qy 361 IPGVSSGLSRMGAVPMVPAQSQAGSLV 390  
Db 361 IPGVSSGLSRMGAVPMVPAQSQAGSLV 390

RESULT 4  
Q925F2 ID Q925F2 PRELIMINARY; PRT; 394 AA.  
AC Q925F2;  
DT 01-DEC-2001 (TRENBLrel. 19, Created)  
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SWISS WEBSTER/NIH;  
RX MEDLINE=21238298; PubMed=11279107;  
RA Hirata K.-I., Ishida T., Penta K., Rezaee M., Yang E., Wohlgenuth J.,  
RA Quertermous T.;  
RT "Cloning of an immunoglobulin family adhesion molecule selectively  
RT expressed by endothelial cells.";  
RL J. Biol. Chem. 276:16223-16231(2001).  
DR EMBL; AF361882; AAK51504.1; --  
SQ SEQUENCE 394 AA; 41810 MW; 3D2B354943A2227D CRC64;

Query Match 69.4%; Score 1397; DB 11; Length 394;  
Best Local Similarity 72.3%; Pred. No. 1.1e-105;  
Matches 285; Conservative 33; Mismatches 72; Indels 4; Gaps 3;

Qy 1 MISLPGLVTLNLLRFLGLSALAPPSRAQLQLHLP--ANRLQAVEGGEVLPWYTLHG 58  
Db 1 MILQAGTPETSLRLVFLGLSTLAAPSAQMBELHVPGLNKLAEVGEVLPWYTTMAR 60  
Qy 59 EVSSQPEVFPVMWFFKQEKEDQVLSYINGVTTSKPGVSLVYMPGRNLSRLGLEQ 117  
Db 61 BESWSHPREVPIILWFLEQEGEPNQLSYINGVMTNKGPTALVHSISRNVSRLGALQ 120  
Qy 118 EKDSGYSCSVNVQDKGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGVANVTLSCOSP 177  
Db 121 EGDGTYRCVNVQNDGKSGHSIKSIELKVLVPPAPPSCSLQGVYVGTNVTNCKSP 180  
Qy 178 RSKPAVOYQWDRQLPSFQTFPAPALDVIRGSLTLNLSMAGVYVCKAHNEVGTACNV 237  
Db 181 RSKPTAQYQWERLAPSSQVFFGFPALDAVRSGLKTLNLSIAMSGLVYVCKAQRVGFACNV 240  
Qy 238 TLEVSTGPGAAVAGAVVGTGLGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWP 297  
Db 241 TLDVMTGSKAAVAGAVVGTGLGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWP 300  
Qy 298 PKSDTISKNGTLSSVTSARALRPPH-GPPRPGALTPPSSQALPSPRLPTTGDGAPQ 356  
Db 301 TKGSDTISKNGTLSSVTSARALRPPHPPGALTPPSSQALPSPRLPTTGDGAPQ 360  
Qy 357 PISPIPGVSSGLSRMGAVPMVPAQSQAGSLV 390  
Db 361 AVSLTPGVSSGLSRMGAVPMVPAQSQAGSLV 394

RESULT 5  
Q9D7I2 ID Q9D7I2 PRELIMINARY; PRT; 204 AA.  
AC Q9D7I2;  
DT 01-JUN-2001 (TRENBLrel. 17, Created)

